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OM protein - protein search, using sw model

Run on: March 3, 2004, 10:27:20 ; Search time 20.3333 Seconds  
(without alignments)  
309.756 Million cell updates/sec

Title: US-09-987-485a-1  
Perfect score: 615  
Sequence: 1 MKLKVNTGTAIDVDVDVK.....KVLVKERDAVQGGGLIKIG 122

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues  
Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/prodata/2/iaa/5A COMB.pep: \*  
2: /cgn2\_6/prodata/2/iaa/5B COMB.pep: \*  
3: /cgn2\_6/prodata/2/iaa/6A COMB.pep: \*  
4: /cgn2\_6/prodata/2/iaa/6B COMB.pep: \*  
5: /cgn2\_6/prodata/2/iaa/PCTUS COMB.pep: \*  
6: /cgn2\_6/prodata/2/iaa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	615	100.0	124	US-09-364-083-2	Sequence 2, Appli
2	615	100.0	124	US-09-651-419-2	Sequence 2, Appli
3	604.5	98.3	123	US-07-956-700B-107	Sequence 107, App
4	604.5	98.3	123	US-08-476-537-107	Sequence 107, App
5	604.5	98.3	123	US-08-485-607-107	Sequence 107, App
6	604.5	98.3	123	US-08-475-879-107	Sequence 107, App
7	604.5	98.3	123	US-07-687-819-1	Sequence 1, Appli
8	604.5	98.3	123	US-09-433-043B-107	Sequence 107, App
9	598.5	97.3	123	US-09-433-043B-128	Sequence 128, App
10	518.5	84.3	106	5252466-6	Patent No. 5252466
11	310	50.4	66	5252466-1	Patent No. 5252466
12	211	34.3	43	US-07-687-819-2	Sequence 2, Appli
13	202.5	32.9	170	US-09-433-043B-127	Sequence 127, App
14	200.5	32.6	165	US-07-956-700B-106	Sequence 106, App
15	200.5	32.6	165	US-08-476-537-106	Sequence 106, App
16	200.5	32.6	165	US-08-485-607-106	Sequence 106, App
17	200.5	32.6	165	US-08-475-879-106	Sequence 106, App
18	200.5	32.6	165	US-09-433-043B-106	Sequence 106, App
19	193.5	31.5	100	5252466-19	Patent No. 5252466
20	175.5	28.5	147	US-09-134-000C-6221	Sequence 6221, App
21	168.5	27.4	612	US-09-252-991A-19134	Sequence 19134, A
22	159.5	25.9	1140	US-09-220-081-2	Sequence 2, Appli
23	159.5	25.9	1140	US-09-677-575-2	Sequence 2, Appli
24	153	24.9	652	US-09-328-352-5587	Sequence 5587, App
25	152	24.7	701	US-09-252-991A-27999	Sequence 27999, A
26	150	24.4	108	US-08-997-080-166	Sequence 166, App
27	150	24.4	108	US-08-997-362-166	Sequence 166, App

28	150	24.4	108	3	US-09-095-855-166	Sequence 166, App
29	150	24.4	108	4	US-09-324-542-166	Sequence 166, App
30	150	24.4	108	4	US-09-205-426-166	Sequence 166, App
31	150	24.4	190	4	US-09-107-532A-5720	Sequence 5720, App
32	150	24.4	243	3	US-09-095-855-199	Sequence 199, App
33	150	24.4	243	4	US-09-205-426-199	Sequence 199, App
34	149	24.2	1154	4	US-09-134-001C-3428	Sequence 3428, App
35	148.5	24.1	676	4	US-09-252-991A-26143	Sequence 26143, A
36	147	23.9	117	4	US-09-673-395A-230	Sequence 230, App
37	144	23.4	1163	4	US-09-134-000C-5707	Sequence 5707, App
38	139.5	22.7	168	4	US-09-134-000C-4552	Sequence 4552, App
39	137	22.3	67	6	5252466-5	Patent No. 5252466
40	136.5	22.2	158	1	US-08-611-107-4	Sequence 4, Appli
41	136.5	22.2	158	2	US-08-422-560A-4	Sequence 4, Appli
42	136.5	22.2	158	3	US-08-468-793-4	Sequence 4, Appli
43	133	21.6	257	1	US-07-956-700B-105	Sequence 105, App
44	133	21.6	257	1	US-08-476-537-105	Sequence 105, App
45	133	21.6	257	1	US-08-485-607-105	Sequence 105, App

ALIGNMENTS

RESULT 1

US-09-364-083-2  
; Sequence 2, Application US/09364083  
; Patent No. 6210676  
; GENERAL INFORMATION:  
; APPLICANT: Callister, Steven M  
; APPLICANT: Lovrich, Steven D  
; APPLICANT: Schell, Ronald F  
; APPLICANT: Jobe, Dean A  
; TITLE OF INVENTION: Compositions and Method Using the Borreliaacidal  
; TITLE OF INVENTION: Epitope(s) of Borrelia burgdorferi Outer Surface  
; TITLE OF INVENTION: Protein C (OspC) for the Diagnosis and Prevention of  
; TITLE OF INVENTION: Lyme Disease  
; FILE REFERENCE: B. burgdorferi, OspC  
; CURRENT APPLICATION NUMBER: US/09/364,083  
; CURRENT FILING DATE: 1999-07-30  
; EARLIER APPLICATION NUMBER: 60/094,955  
; EARLIER FILING DATE: 1998-07-31  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 194  
; TYPE: PRT  
; ORGANISM: Borrelia burgdorferi  
US-09-364-083-2

Query Match 100.0%; Score 615; DB 3; Length 194;  
Best Local Similarity 100.0%; Pred. No. 2.8e-57;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLKVNTGTAIDVDVDVKSHENPMGTILFGGTGGAPAPAGGAGKAGEIAPL 60  
Db 1 MKLKVNTGTAIDVDVDVKSHENPMGTILFGGTGGAPAPAGGAGKAGEIAPL 60  
QY 61 AGTWSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVKVLVKERDAVQGGGLIK 120  
Db 61 AGTWSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVKVLVKERDAVQGGGLIK 120  
QY 121 IG 122  
Db 121 IG 122

RESULT 2

US-09-651-419-2  
; Sequence 2, Application US/09651419  
; Patent No. 6464985  
; GENERAL INFORMATION:  
; APPLICANT: Callister, Steven M  
; APPLICANT: Lovrich, Steven D

APPLICANT: Schell, Ronald F  
APPLICANT: Jobe, Dean A  
TITLE OF INVENTION: Compositions and Method Using the Borreliaacidal  
TITLE OF INVENTION: Epitope(s) of Borrelia burgdorferi Outer Surface  
TITLE OF INVENTION: Protein C (OspC) for the Diagnosis and Prevention of  
TITLE OF INVENTION: Lyme Disease  
FILE REFERENCE: B. burgdorferi  
CURRENT APPLICATION NUMBER: US/09/651.419  
CURRENT FILING DATE: 2000-08-30  
PRIOR APPLICATION NUMBER: 60/094,955  
PRIOR FILING DATE: 1998-07-31  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 194  
TYPE: PRT  
ORGANISM: Borrelia burgdorferi  
US-09-651-419-2

Query Match 100.0%; Score 615; DB 4; Length 194;  
Best Local Similarity 100.0%; Pred. No. 2.8e-57;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLKVTVNGTAYDVEDVDVKSHENPMGTILFGGTTGGAPAPAAAGGAGAGKAGEGEIPAPL 60  
DB 1 MKLKVTVNGTAYDVEDVDVKSHENPMGTILFGGTTGGAPAPAAAGGAGAGKAGEGEIPAPL 60  
QY 61 AGTWSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKLVKRDVAVGGQGLIK 120  
DB 61 AGTWSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKLVKRDVAVGGQGLIK 120  
QY 121 IG 122  
DB 121 IG 122

RESULT 3  
US-07-956-700B-107  
Sequence 107, Application US/07956700B  
Patent No. 5539092  
GENERAL INFORMATION:  
APPLICANT: Robert Haselkorn and Piotr Gornicki  
TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
TITLE OF INVENTION: Carboxylase  
NUMBER OF SEQUENCES: 116  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: 321 No. 5539092th Clark Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60610  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/956,700B  
FILING DATE: 19921002  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Thomas E. No. 5539092thrup  
REGISTRATION NUMBER: 33,268  
REFERENCE/DOCKET NUMBER: ARCD:058  
TELEPHONE: 1-312-744-0090  
TELEFAX: 1-312-755-4489  
INFORMATION FOR SEQ ID NO: 107:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: Amino acid  
STRANDEDNESS: Single

TOPOLOGY: Linear  
MOLECULE TYPE: Peptide  
US-07-956-700B-107  
Query Match 98.3%; Score 604.5; DB 1; Length 123;  
Best Local Similarity 99.2%; Pred. No. 2e-56;  
Matches 122; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MKLKVTVNGTAYDVEDVDVKSHENPMGTILFGGTTGGAPAPAAAGGAGAGKAGEGEIPAP 59  
DB 1 MKLKVTVNGTAYDVEDVDVKSHENPMGTILFGGTTGGAPAPAAAGGAGAGKAGEGEIPAP 60  
QY 60 LAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKLVKRDVAVGGQGLI 119  
DB 61 LAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKLVKRDVAVGGQGLI 120  
QY 120 KIG 122  
DB 121 KIG 123

RESULT 4  
US-08-476-537-107  
Sequence 107, Application US/08476537  
Patent No. 5756290  
GENERAL INFORMATION:  
APPLICANT: Robert Haselkorn and Piotr Gornicki  
TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
TITLE OF INVENTION: Carboxylase  
NUMBER OF SEQUENCES: 116  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: 321 No. 5756290th Clark Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60610  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,537  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/956,700  
FILING DATE: 10/21/92  
ATTORNEY/AGENT INFORMATION:  
NAME: Thomas E. No. 5756290thrup  
REGISTRATION NUMBER: 33,268  
REFERENCE/DOCKET NUMBER: ARCD:058  
TELEPHONE: 1-312-744-0090  
TELEFAX: 1-312-755-4489  
INFORMATION FOR SEQ ID NO: 107:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 123 amino acids  
TYPE: Amino acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Peptide  
US-08-476-537-107

Query Match 98.3%; Score 604.5; DB 1; Length 123;  
Best Local Similarity 99.2%; Pred. No. 2e-56;  
Matches 122; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MKLKVTVNGTAYDVEDVDVKSHENPMGTILFGGTTGGAPAPAAAGGAGAGKAGEGEIPAP 59  
DB 1 MKLKVTVNGTAYDVEDVDVKSHENPMGTILFGGTTGGAPAPAAAGGAGAGKAGEGEIPAP 60

[illegible]

## RESULT 5

```

US-08-485-607-107
; Sequence 107, Application US/08485607
; Patent No. 5792627
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5792627th Clark Street
; City: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610

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Query Match 98.3%; Score 604.5; DB 1; Length 123;  
Best Local Similarity 99.2%; Pred. No. 2e-56;  
Matches 122; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY	60	L	A	G	T	V	K	S	K	I	L	V	K	E	G	D	T	V	K	A	G	T	V	L	E	A	M	K	M	E	T	E	I	N	A	P	T	D	G	K	V	E	K	V	L	V	K	E	R	D	A	V	Q	G	G	L	I	119
DB	61	L	A	G	T	V	K	S	K	I	L	V	K	E	G	D	T	V	K	A	G	T	V	L	E	A	M	K	M	E	T	E	I	N	A	P	T	D	G	K	V	E	K	V	L	V	K	E	R	D	A	V	Q	G	G	L	I	120
QY	120	K	I	G	122																																																					
DB	121	K	I	G	123																																																					

## RESULT 6

US-08-475-879-107  
; Sequence 107, Application US/08475879

; Patent No. 5972644  
 ; Patent No. 5972644 5786170  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Robert Hasselkorn and Piotr Gornicki  
 ; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
 ; TITLE OF INVENTION: Carboxylase  
 ; NUMBER OF SEQUENCES: 116  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Arnold, White & Durkee  
 ; STREET: 321 No. 5972644 5786170th Clark Street  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60610  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy Disk  
 ; COMPUTER: IBM PC Compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: ASCII-DOS  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/475,879  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/956,700  
 ; FILING DATE: 10/21/92  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Thomas E. No. 5972644 5786170thrup  
 ; REGISTRATION NUMBER: 33,268  
 ; REFERENCE/DOCKET NUMBER: ARCD:058  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 1-312-744-0090  
 ; TELEFAX: 1-312-755-4489  
 ; INFORMATION FOR SEQ ID NO: 107:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 123 amino acids  
 ; TYPE: Amino acid  
 ; STRANDEDNESS: Single  
 ; TOPOLOGY: Linear  
 ; MOLECULE TYPE: Peptide  
 ; US-08-475-879-107

Query Match	98.3%	Score 604.5	DB 2	Length 123
Best Local Similarity	99.2%	Pred. No. 2e-56		
Matches 122	Conservative	0	Mismatches 0	Indels 1
Matches 122	Conservative	0	Mismatches 0	Indels 1
Matches 122	Conservative	0	Mismatches 0	Indels 1

[illegible]

## RESULT 7

US-07-687-819-1  
; Sequence 1, Application US/07687819  
; Patent No. 6822439  
; GENERAL INFORMATION:  
; APPLICANT: Haase, Ferdinand C.  
; APPLICANT: Cress, Dean E.  
; TITLE OF INVENTION: Carrier Protein  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADRESSE: Rohm and Haas Company  
; STREET: Independence Mall West  
; CITY: Philadelphia  
; STATE: PA

COUNTRY: USA  
 ZIP: 13105  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/687,819  
 FILING DATE: 19910520  
 CLASSIFICATION: 530  
 CLASSIFICATION: C07K13/00  
 CLASSIFICATION: C07K15/26  
 CLASSIFICATION: C12P21/00  
 CLASSIFICATION: 424/85.7  
 CLASSIFICATION: 530/351  
 CLASSIFICATION: 435/69.51  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Driks, Jordan J.  
 REGISTRATION NUMBER: 22,029  
 REFERENCE/DOCKET NUMBER: 89-020  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 215-592-2478  
 TELEFAX: 215-592-2682  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 123 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE:  
 ORGANISM: Propionibacterium shermanii  
 PUBLICATION INFORMATION:  
 AUTHORS: Malov, W L  
 AUTHORS: Bowien, B U  
 AUTHORS: Zwolinski, G K  
 AUTHORS: Kumar, K G  
 AUTHORS: Wood, H G  
 TITLE: Amino Acid Sequence of the Biotinyl Subunit  
 Patent No. 6072039  
 TITLE: from Transcarboxylase  
 JOURNAL: Journal of Biological Chemistry  
 VOLUME: 254  
 ISSUE: 22  
 PAGES: 11615-11622  
 DATE: NO. 6072039 26-1979  
 RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 123  
 US-07-687-819-1  
 Query Match 98.3%; Score 604.5; DB 3; Length 123;  
 Best Local Similarity 99.2%; Pred. No. 2e-56;  
 Matches 122; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 MKLKVTVNGTAYDVDVDKSHENPMGTILFGGTTGGAPAP-AAGGAGAGKAGEGEIPAP 59  
 Db 1 MKLKVTVNGTAYDVDVDKSHENPMGTILFGGTTGGAPAPRAAGGAGAGKAGEGEIPAP 60  
 QY 60 LAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGGLI 119  
 Db 61 LAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGGLI 120  
 QY 120 KIG 122  
 Db 121 KIG 123  
 RESULT 8  
 US-09-433-043B-107  
 ; Sequence 107, Application US/09433043B  
 ; Patent No. 6399342  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HASELKORN, ROBERT  
 ; APPLICANT: GORNICKI, PIOTR  
 ; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE  
 ; FILE REFERENCE: ARCD:338US  
 ; CURRENT APPLICATION NUMBER: US/09/433,043B  
 ; CURRENT FILING DATE: 1999-10-25  
 ; PRIOR APPLICATION NUMBER: 08/475,879  
 ; PRIOR FILING DATE: 1995-06-07  
 ; PRIOR APPLICATION NUMBER: 07/956,700  
 ; PRIOR FILING DATE: 1992-10-02  
 ; NUMBER OF SEQ ID NOS: 128  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 128  
 ; LENGTH: 123  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Peptide  
 ; US-09-433-043B-107  
 Query Match 97.3%; Score 598.5; DB 4; Length 123;  
 Best Local Similarity 98.4%; Pred. No. 8.6e-56;  
 Matches 121; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
 QY 1 MKLKVTVNGTAYDVDVDKSHENPMGTILFGGTTGGAPAP-AAGGAGAGKAGEGEIPAP 59  
 Db 1 MKLKVTVNGTAYDVDVDKSHENPMGTILFGGTTGGAPAPRAAGGAGAGKAGEGEIPAP 60  
 QY 60 LAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGGLI 119  
 Db 61 LAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGGLI 120  
 QY 120 KIG 122  
 Db 121 KIG 123  
 RESULT 9  
 US-09-433-043B-128  
 ; Sequence 128, Application US/09433043B  
 ; Patent No. 6399342  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HASELKORN, ROBERT  
 ; APPLICANT: GORNICKI, PIOTR  
 ; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE  
 ; FILE REFERENCE: ARCD:338US  
 ; CURRENT APPLICATION NUMBER: US/09/433,043B  
 ; CURRENT FILING DATE: 1999-10-25  
 ; PRIOR APPLICATION NUMBER: 08/475,879  
 ; PRIOR FILING DATE: 1995-06-07  
 ; PRIOR APPLICATION NUMBER: 07/956,700  
 ; PRIOR FILING DATE: 1992-10-02  
 ; NUMBER OF SEQ ID NOS: 128  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 128  
 ; LENGTH: 123  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Peptide  
 ; US-09-433-043B-128  
 Query Match 97.3%; Score 598.5; DB 4; Length 123;  
 Best Local Similarity 98.4%; Pred. No. 8.6e-56;  
 Matches 121; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
 QY 1 MKLKVTVNGTAYDVDVDKSHENPMGTILFGGTTGGAPAP-AAGGAGAGKAGEGEIPAP 59  
 Db 1 MKLKVTVNGTAYDVDVDKSHENPMGTILFGGTTGGAPAPRAAGGAGAGKAGEGEIPAP 60  
 QY 60 LAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGGLI 119  
 Db 61 LAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGGLI 120  
 QY 120 KIG 122  
 Db 121 KIG 123



QY 120 KIG 122  
Db 121 HIG 123

## RESULT 10

5252466-6

; Patent No. 5252466

; APPLICANT: CRONAN, JOHN E.

; TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN

; VIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND

; PURIFYING THEM

; NUMBER OF SEQUENCES: 24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/525,568

; FILING DATE: 18-MAY-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 354,266

; FILING DATE: 19-MAY-1989

; SEQ ID NO: 6:

; LENGTH: 106

5252466-6

## Query Match

Best Local Similarity 84.3%; Score 518.5; DB 6; Length 106;

Matches 105; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 18 VDKSHENPMGTTILFGGTTGGAPAP-AAGGAGAGKAGEGEIPAPLAGTWSKILVKEGDTVK 76  
Db 1 VDKSHENPMGTTILFGGTTGGAPAPRAAGAGAGKAGEGEIPAPLAGTWSKILVKEGDTVK 60

QY 77 AGQTVLVEAMKMETEINAPTQGVKVLVKERDAVQGGGLIKIG 122  
Db 61 AGQTVLVEAMKMETEINAPTQGVKVLVKERDAVQGGGLIKIG 106

## RESULT 11

5252466-1

; Patent No. 5252466

; APPLICANT: CRONAN, JOHN E.

; TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN

; VIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND

; PURIFYING THEM

; NUMBER OF SEQUENCES: 24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/525,568

; FILING DATE: 18-MAY-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 354,266

; FILING DATE: 19-MAY-1989

; SEQ ID NO: 1:

; LENGTH: 66

5252466-1

## Query Match

Best Local Similarity 50.4%; Score 310; DB 6; Length 66;

Matches 64; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 57 PAPLAGTWSKILVKEGDTVKAGQTVLVEAMKMETEINAPTQGVKVLVKERDAVQGGQ 116  
Db 1 PAPLAGTWSKILVKEGDTVKAGQTVLVEAMKMETEINAPTQGVKVLVKERDAVQGGQ 60

QY 117 GLIKIG 122  
Db 61 GLIKIG 66

## RESULT 12

US-07-687-819-2

; Sequence 2, Application US/07687819

; Patent No. 6072039

; GENERAL INFORMATION:

; APPLICANT: Haase, Ferdinand C.  
; APPLICANT: Cress, Dean E.  
; TITLE OF INVENTION: Carrier Protein  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rohm and Haas Company  
; STREET: Independence Mall West  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/07/687,819  
; APPLICATION NUMBER: 19910520  
; FILING DATE: 19910520  
; CLASSIFICATION: 530  
; CLASSIFICATION: C07K13/00  
; CLASSIFICATION: C07K15/26  
; CLASSIFICATION: C12P21/00  
; CLASSIFICATION: 424/85.7  
; CLASSIFICATION: 530/351  
; CLASSIFICATION: 435/69.51  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Driks, Jordan J.  
; REGISTRATION NUMBER: 22,029  
; REFERENCE/DOCKET NUMBER: 89-020  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-592-2478  
; TELEFAX: 215-592-2682  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 43 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; US-07-687-819-2

Query Match 34.3%; Score 211; DB 3; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.5e-15;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 PAPLAGTWSKILVKEGDTVKAGQTVLVEAMKMETEINAPTQGV 99  
Db 1 PAPLAGTWSKILVKEGDTVKAGQTVLVEAMKMETEINAPTQGV 43

## RESULT 13

US-09-433-043B-127

; Sequence 127, Application US/09433043B

; Patent No. 6399342

; GENERAL INFORMATION:

; APPLICANT: HASELKORN, ROBERT

; APPLICANT: GORNICKI, PIOTR

; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE

; FILE REFERENCE: ARCD:338US

; CURRENT APPLICATION NUMBER: US/09/433,043B

; CURRENT FILING DATE: 1999-10-25

; PRIOR APPLICATION NUMBER: 08/475,879

; PRIOR FILING DATE: 1995-06-07

; PRIOR APPLICATION NUMBER: 07/956,700

; PRIOR FILING DATE: 1992-10-02

; NUMBER OF SEQ ID NOS: 128

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 127

; LENGTH: 170

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-433-043B-127

Query Match 32.9%; Score 202.5; DB 4; Length 170;  
Best Local Similarity 52.9%; Pred. No. 6.8e-14;  
Matches 45; Conservative 10; Mismatches 29; Indels 1; Gaps 1;  
  
Qy 38 APAPAGGAGKAGGEG-EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAP 96  
Db 85 APAPASAPAAAAPAGAGTPTVAPLAGTIWKVLASEGQTVAAAGEVLLILEAMKMETEIRAA 144  
  
Qy 97 TDGKVEKLVKRDVAVQGGGLIKI 121  
Db 145 QAGTVRGIAVKAGDAVAVGDTLMTL 169

RESULT 14  
US-07-956-700B-106  
; Sequence 106, Application US/07956700B  
; Patent No. 5539092  
; GENERAL INFORMATION:  
; APPLICANT: Robert Haselkorn and Piotr Gornicki  
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
; TITLE OF INVENTION: Carboxylase  
; NUMBER OF SEQUENCES: 116  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 321 No. 5539092th Clark Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60610  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII-DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/956,700B  
; FILING DATE: 19921002  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Thomas E. No. 5539092thrup  
; REGISTRATION NUMBER: 33,268  
; REFERENCE/DOCKET NUMBER: ARCD:058  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 1-312-744-0090  
; TELEFAX: 1-312-755-4489  
; INFORMATION FOR SEQ ID NO: 106:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 165 amino acids  
; TYPE: Amino acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; MOLECULE TYPE: Peptide  
US-07-956-700B-106

Query Match 32.6%; Score 200.5; DB 1; Length 165;  
Best Local Similarity 52.9%; Pred. No. 1.1e-13;  
Matches 45; Conservative 10; Mismatches 29; Indels 1; Gaps 1;  
  
Qy 38 APAPAGGAGKAGGEG-EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAP 96  
Db 80 APAPASAPAAAAPAGAGTPTVAPLAGTIWKVLASEGQTVAAAGEVLLILEAMKMETEIRAA 139  
  
Qy 97 TDGKVEKLVKRDVAVQGGGLIKI 121  
Db 140 QAGTVRGIAVKAGDAVAVGDTLMTL 164

RESULT 15  
US-08-476-537-106

; Sequence 106, Application US/08476537  
; Patent No. 5756290  
; GENERAL INFORMATION:  
; APPLICANT: Robert Haselkorn and Piotr Gornicki  
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
; TITLE OF INVENTION: Carboxylase  
; NUMBER OF SEQUENCES: 116  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 321 No. 5756290th Clark Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60610  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII-DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/476,537  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/956,700  
; FILING DATE: 10/21/92  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Thomas E. No. 5756290thrup  
; REGISTRATION NUMBER: 33,268  
; REFERENCE/DOCKET NUMBER: ARCD:058  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 1-312-744-0090  
; TELEFAX: 1-312-755-4489  
; INFORMATION FOR SEQ ID NO: 106:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 165 amino acids  
; TYPE: Amino acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; MOLECULE TYPE: Peptide  
US-08-476-537-106

Query Match 32.6%; Score 200.5; DB 1; Length 165;  
Best Local Similarity 52.9%; Pred. No. 1.1e-13;  
Matches 45; Conservative 10; Mismatches 29; Indels 1; Gaps 1;  
  
Qy 38 APAPAGGAGKAGGEG-EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAP 96  
Db 80 APAPASAPAAAAPAGAGTPTVAPLAGTIWKVLASEGQTVAAAGEVLLILEAMKMETEIRAA 139  
  
Qy 97 TDGKVEKLVKRDVAVQGGGLIKI 121  
Db 140 QAGTVRGIAVKAGDAVAVGDTLMTL 164

RESULT 16  
US-08-485-607-106  
; Sequence 106, Application US/08485607  
; Patent No. 5792627  
; GENERAL INFORMATION:  
; APPLICANT: Robert Haselkorn and Piotr Gornicki  
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
; TITLE OF INVENTION: Carboxylase  
; NUMBER OF SEQUENCES: 116  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 321 No. 5792627th Clark Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60610  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk

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;
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,607
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5792627thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-08-485-607-106

Query Match 32.6%; Score 200.5; DB 1; Length 165;
Best Local Similarity 52.9%; Pred. No. 1.1e-13;
Matches 45; Conservative 10; Mismatches 29; Indels 1; Gaps 1;

QY 38 APAPAGGAGAGKAGGEG-EIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAP 96
Db 80 APAPASAPAAAAPAGAGTPTAPLAGTIWKVLASEGQTVAAAGEVLLILEAMKMETEIRAA 139

QY 97 TDGKVEKVLKRDVAVGGQGLIKI 121
Db 140 QAGTVRGIAVKAGDAVAVGDTLMTL 164

RESULT 17
US-08-475-879-106
; Sequence 106, Application US/08/475,879
; Patent No. 5972644
; Patent No. 5972644 5786170
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Arnold, White & Durkee
; STREET: 321 No. 5972644 5786170th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,879
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5972644 5786170thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
```

```
;
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-08-475-879-106

Query Match 32.6%; Score 200.5; DB 2; Length 165;
Best Local Similarity 52.9%; Pred. No. 1.1e-13;
Matches 45; Conservative 10; Mismatches 29; Indels 1; Gaps 1;

QY 38 APAPAGGAGAGKAGGEG-EIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAP 96
Db 80 APAPASAPAAAAPAGAGTPTAPLAGTIWKVLASEGQTVAAAGEVLLILEAMKMETEIRAA 139

QY 97 TDGKVEKVLKRDVAVGGQGLIKI 121
Db 140 QAGTVRGIAVKAGDAVAVGDTLMTL 164

RESULT 18
US-09-433-043B-106
; Sequence 106, Application US/09/433043B
; Patent No. 8399342
; GENERAL INFORMATION:
; APPLICANT: HASELKORN, ROBERT
; APPLICANT: GORNICKI, PIOTR
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
; FILE REFERENCE: ARCD:338US
; CURRENT APPLICATION NUMBER: US/09/433,043B
; CURRENT FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/475,879
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/956,700
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
; US-09-433-043B-106

Query Match 32.6%; Score 200.5; DB 4; Length 165;
Best Local Similarity 52.9%; Pred. No. 1.1e-13;
Matches 45; Conservative 10; Mismatches 29; Indels 1; Gaps 1;

QY 38 APAPAGGAGAGKAGGEG-EIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAP 96
Db 80 APAPASAPAAAAPAGAGTPTAPLAGTIWKVLASEGQTVAAAGEVLLILEAMKMETEIRAA 139

QY 97 TDGKVEKVLKRDVAVGGQGLIKI 121
Db 140 QAGTVRGIAVKAGDAVAVGDTLMTL 164

RESULT 19
5252466-19
; Patent No. 5252466
; APPLICANT: CRONAN, JOHN E.
; TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN
; VIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND
; PURIFYING THEM
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/525,568
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; FILING DATE: 18-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 354,266
; FILING DATE: 19-MAY-1989
; SEQ ID NO:19:
; LENGTH: 100
5252466-19

Query Match
Best Local Similarity 31.5%; Score 193.5; DB 6; Length 100;
Matches 44; Conservative 10; Mismatches 30; Indels 1; Gaps 1;

QY 38 APAPAGGAGAGKAGSG-EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAP 96
Db 15 APAPASAPAAAPAGAGTPTAPLAGFINKVLASEGQTVAAAGEVLLILEAMKMETEIRAA 74
QY 97 TDCKVEKVLKRDVAVQGGGLIKI 121
Db 75 QAGTVRGIAVKAGDAVAVGDTLMTL 99

RESULT 20
US-09-134-000C-6221
; Sequence 6221, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6221
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6221

Query Match
Best Local Similarity 28.5%; Score 175.5; DB 4; Length 147;
Matches 48; Conservative 17; Mismatches 55; Indels 9; Gaps 2;

QY 2 KLVTVNGTAYDVIDV-----VDKSHENPMGTILFGGGTGGAPA-----PAAGGAGAGKAG 52
Db 18 KFKISIDGKVLVMEERIGGVQPAPVAPQPTAPVATTETAPAVETFPASAAQPAAPAG 77
QY 53 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTGDGKVEKVLKRDV 112
Db 78 ADAMPAPMPGTVLKVLNVNGDTSENOPLLILEAMKMETEIVAGKAGTGTGIHVTQGGIV 137
QY 113 QGGGLIKI 121
Db 138 NPGELITI 146

RESULT 21
US-09-252-991A-19134
; Sequence 19134, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190

; FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19134
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19134

Query Match
Best Local Similarity 27.4%; Score 168.5; DB 4; Length 612;
Matches 44; Conservative 20; Mismatches 43; Indels 29; Gaps 3;

QY 5 VTVNGTAYDVIDV-----DVKXSGH-----NPMGTILFGGGTGGAPAPAGG 45
Db 485 IDVHGETYVDITGVGKSDNKRHFVLSIDGMPFVWFPELVNEYVAGSASGRKHA----- 539
QY 46 AGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTGDGKVEKVL 105
Db 540 -----SEPGHVSITMPGNTVDVLVKEGDSVKAGQAVLITAMKMETEVOAGIAGTVKAIH 594
QY 106 VKERDAVQGGGLIKI 121
Db 595 VAKGDRVNPGEILIEI 610

RESULT 22
US-09-220-081-2
; Sequence 2, Application US/09220081
; Patent No. 6171833
; GENERAL INFORMATION:
; APPLICANT: Sinskey, Anthony J.
; APPLICANT: Lessard, Philip A.
; APPLICANT: Willis, Laura B.
; APPLICANT: Stephanopoulos, Gregory
; TITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum
; FILE REFERENCE: 1533.0790000
; CURRENT APPLICATION NUMBER: US/09/220,081
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1140
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-220-081-2

Query Match
Best Local Similarity 25.9%; Score 159.5; DB 3; Length 1140;
Matches 32; Conservative 15; Mismatches 26; Indels 1; Gaps 1;

QY 48 AGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTGDGKVEKVLK 107
Db 1067 ADSNKGSHVAPGAGVVT-VTVAGGDEVKAGDAVAIIEMKMEATITASVDGKIDRVVVP 1125
QY 108 ERDAVQGGGLIKI 121
Db 1126 AATKVEGGDLIVVV 1139

RESULT 23
US-09-677-575-2
; Sequence 2, Application US/09677575
; Patent No. 6403351
; GENERAL INFORMATION:
; APPLICANT: Sinskey, Anthony J.
; APPLICANT: Lessard, Philip A.
; APPLICANT: Willis, Laura B.
; APPLICANT: Stephanopoulos, Gregory
; TITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum
; FILE REFERENCE: 1533.0790000
; CURRENT APPLICATION NUMBER: US/09/677,575
; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 09/220,081
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; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1140  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-09-677-575-2

Query Match 25.9%; Score 159.5; DB 4; Length 1140;  
Best Local Similarity 43.2%; Pred. No. 2.5e-08;  
Matches 32; Conservative 15; Mismatches 26; Indels 1; Gaps 1;  
Qy 48 AGKAGEGEIPAPLAGTYSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVK 107  
Db 1067 ADSNKGHVAAPFAGVVT-VTVAEGDEVKAGDAVAILIEMKMEATITASVDGKIDRVVP 1125

Qy 108 ERDAVQGGGLIKI 121  
Db 1126 AATKVEGGDLIVVV 1139

## RESULT 24

US-09-328-352-5587  
; Sequence 5587, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 5587  
; LENGTH: 652  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-5587

Query Match 24.9%; Score 153; DB 4; Length 652;  
Best Local Similarity 45.9%; Pred. No. 6.1e-08;  
Matches 34; Conservative 15; Mismatches 25; Indels 0; Gaps 0;  
Qy 48 AGKAGEGEIPAPLAGTYSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVK 107  
Db 577 ADVAGDKIRAPMDGAVNVILNKGQVKGQTLVLVLEAMKIQQIKSDVDGVDEILGQ 636

Qy 108 ERDAVQGGGLIKI 121  
Db 637 QGQGVKKRQMLFSI 650

## RESULT 25

US-09-252-991A-27999  
; Sequence 27999, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 27999  
; LENGTH: 701  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa

## US-09-252-991A-27999

Query Match 24.7%; Score 152; DB 4; Length 701;  
Best Local Similarity 42.1%; Pred. No. 8.5e-08;  
Matches 32; Conservative 18; Mismatches 26; Indels 0; Gaps 0;  
Qy 46 AGKAGEGEIPAPLAGTYSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVL 105  
Db 621 AEAHAHQGLSAPMNGSIVRLVPEQTVVEAGATLVLEAMKMEHSIRAPHAGVVVKALY 680  
Qy 106 VKERDAVQGGGLIKI 121  
Db 681 CSEGELVEEGTFLVEL 696

## RESULT 26

US-08-997-080-166  
; Sequence 166, Application US/08997080  
; Patent No. 5968524  
; GENERAL INFORMATION:  
; APPLICANT: WATSON, JAMES D.  
; APPLICANT: TAN, PAUL L.J.  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-  
; NUMBER OF SEQUENCES: 194  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Ann W. Speckman  
; STREET: 2601 Elliott Avenue, Suite 4185  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/997,080  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sleath, Janet  
; REGISTRATION NUMBER: 37,037  
; REFERENCE/DOCKET NUMBER: 11000.1007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-269-0565  
; TELEFAX: 206-269-0563  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 166:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-997-080-166

Query Match 24.4%; Score 150; DB 2; Length 108;  
Best Local Similarity 46.5%; Pred. No. 1.3e-08;  
Matches 33; Conservative 10; Mismatches 28; Indels 0; Gaps 0;

Qy 52 GEGEIPAPLAGTYSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLKERDA 111  
Db 33 GDERVDAPFASVWKVDVAVGDRVAGQPLALEAMKMETVLRAPADGVVTVQLIVSAGHL 92  
Qy 112 VQGGGLIKIG 122  
Db 93 VDPGTPLVWVG 103

## RESULT 27

```

US-08-997-362-166
; Sequence 166, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 166:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-997-362-166

Query Match 24.4%; Score 150; DB 2; Length 108;
Best Local Similarity 46.5%; Pred. No. 1.3e-08;
Matches 33; Conservative 10; Mismatches 28; Indels 0; Gaps 0;

Qy 52 GEGEIPAPLAGTYSKILVKEGDTVKAGOTVLVLEAMKMETEINAPTDGKVKVLKERDA 111
Db 33 GDERVDAPFASVWKVDVAVGDRVVAGQPLLALAMKMETVLRAPADGVVTQILVSAGHL 92

Qy 112 VQGGQGLIKIG 122
Db 93 VDPGTPLVWVG 103

RESULT 28
US-09-095-855-166
; Sequence 166, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for

```

```

; TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 166:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-095-855-166

Query Match 24.4%; Score 150; DB 3; Length 108;
Best Local Similarity 46.5%; Pred. No. 1.3e-08;
Matches 33; Conservative 10; Mismatches 28; Indels 0; Gaps 0;

Qy 52 GEGEIPAPLAGTYSKILVKEGDTVKAGOTVLVLEAMKMETEINAPTDGKVKVLKERDA 111
Db 33 GDERVDAPFASVWKVDVAVGDRVVAGQPLLALAMKMETVLRAPADGVVTQILVSAGHL 92

Qy 112 VQGGQGLIKIG 122
Db 93 VDPGTPLVWVG 103

RESULT 29
US-09-324-542-166
; Sequence 166, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; of Immunologically-Mediated Skin Disorders
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 166
; LENGTH: 108

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; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-324-542-166

Query Match      24.4%; Score 150; DB 4; Length 108;
Best Local Similarity 46.5%; Pred. No. 1.3e-08;
Matches 33; Conservative 10; Mismatches 28; Indels 0; Gaps 0;

QY 52 GGEIPAPLAGTIVSKILVKEGDTVKAGOTVVLVLEAMKMETEINAPTDGKVEKVLVKERDA 111
DB 33 GDERVDAPFASVWKVDVAVGRVVGQPLLALAEAMKMETVLRAPADGVTQILVSAGHL 92

QY 112 VQGGGLIKIG 122
DB 93 VDPGTPLVVVG 103

RESULT 30
US-09-205-426-166
; Sequence 166, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 166
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-205-426-166

Query Match      24.4%; Score 150; DB 4; Length 108;
Best Local Similarity 46.5%; Pred. No. 1.3e-08;
Matches 33; Conservative 10; Mismatches 28; Indels 0; Gaps 0;

QY 52 GGEIPAPLAGTIVSKILVKEGDTVKAGOTVVLVLEAMKMETEINAPTDGKVEKVLVKERDA 111
DB 33 GDERVDAPFASVWKVDVAVGRVVGQPLLALAEAMKMETVLRAPADGVTQILVSAGHL 92

QY 112 VQGGGLIKIG 122
DB 93 VDPGTPLVVVG 103

RESULT 31
US-09-107-532A-5720
; Sequence 5720, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A. Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
```

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; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5720:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 190 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...190
; SEQUENCE DESCRIPTION: SEQ ID NO: 5720:
US-09-107-532A-5720

Query Match      24.4%; Score 150; DB 4; Length 190;
Best Local Similarity 46.3%; Pred. No. 2.7e-08;
Matches 31; Conservative 13; Mismatches 23; Indels 0; Gaps 0;

QY 55 EIPAPLAGTIVSKILVKEGDTVKAGOTVVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQG 114
DB 121 QIGATMSGVLDVLVKGDNVKGDTLMTETAMKMETALEARFDGKVAHVYVSSGNTISS 180

QY 115 GGLIKI 121
DB 161 GDLIEV 187

RESULT 32
US-09-095-855-199
; Sequence 199, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
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Query Match 24.4%; Score 150; DB 4; Length 2437;  
Best Local Similarity 46.5%; Pred. No. 3.6e-08;  
Matches 33; Conservative 10; Mismatches 28; Indels

RESULT 35  
US-09-252-991A-26143  
; Sequence 26143, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 26143  
; LENGTH: 676  
; TYPE: PRF  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-26143

Query Match 24.1%; Score 148.5; DB 4; Length 676;  
Best Local Similarity 35.7%; Pred. No. 1.9e-07;  
Matches 41; Conservative 16; Mismatches 43; Indels 15; Gaps 2;



QY 11 AYVDVVDKSHENPMGTILFGGTGG-----APAPAGGAGAGAGAGGEIPAPLAGTVSK 66  
Db 569 AYHVD-----GRLWVYGHGNGLELVEVTHAGASAQVGASSGTLKAPMDGAIVE 617  
QY 67 ILVKEGDTVKAGOTVLVLEAMKMETEINAPTDGKVKVVKERDAVGGGGLIKI 121  
Db 618 VLVEGERVKGQLLLVLEAMKMEHLKAGVDGVRRVQVGRGEQVRNRQVLVEV 672

RESULT 36  
US-09-673-395A-230  
; Sequence 230, Application US/09673395A  
; Patent No. 6620923  
; GENERAL INFORMATION:  
; APPLICANT: SPECHT, THOMAS  
; APPLICANT: HINZMANN, BERND  
; APPLICANT: SCHMITT, ARMIN  
; APPLICANT: PILARSKY, CHRISTIAN  
; APPLICANT: DAHL, EDGAR  
; APPLICANT: ROSENTHAL, ANDRE  
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE  
; FILE REFERENCE: ALBRE-12  
; CURRENT APPLICATION NUMBER: US/09/673,395A  
; CURRENT FILING DATE: 2000-10-17  
; NUMBER OF SEQ ID NOS: 637  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 230  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-673-395A-230

Query Match 23.9%; Score 147; DB 4; Length 117;  
Best Local Similarity 42.9%; Pred. No. 3e-08;  
Matches 30; Conservative 14; Mismatches 26; Indels 0; Gaps 0;  
QY 39 PAPAAGGAGAGAGAGGEIPAPLAGTVSKILVKEGDTVKAGOTVLVLEAMKMETEINAPTD 98  
Db 24 PVPKYLSSVSSQETGGGLAPMTGTIEKFVKAGDKVKGDSLWVMIAMKMEHTIKSPKD 83  
QY 99 GKVEKVLVKE 108  
Db 84 GTVKKVFYRE 93

RESULT 37  
US-09-134-000C-5707  
; Sequence 5707, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5707  
; LENGTH: 1163  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-5707

Query Match 23.4%; Score 144; DB 4; Length 1163;  
Best Local Similarity 43.3%; Pred. No. 1.1e-06;  
Matches 29; Conservative 17; Mismatches 21; Indels 0; Gaps 0;  
QY 55 EIPAPLAGTVSKILVKEGDTVKAGOTVLVLEAMKMETEINAPTDGKVKVVKERDAVGG 114

Db 1094 QIGATSGSVLQVLVKEGDKVEKQPIILITEAMKMETTIEARFAGTVDHIVVEGEAISS 1153  
QY 115 GQGLIKI 121  
Db 1154 GDLILEV 1160

RESULT 38  
US-09-134-000C-4552  
; Sequence 4552, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4552  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-4552

Query Match 22.7%; Score 139.5; DB 4; Length 168;  
Best Local Similarity 40.5%; Pred. No. 2.9e-07;  
Matches 30; Conservative 12; Mismatches 25; Indels 7; Gaps 1;  
QY 55 EIPAPLAGTV-----SKILVKEGDTVKAGOTVLVLEAMKMETEINAPTDGKVKVVK 107  
Db 91 EITSPIVIGIVLQAPDPKFNFKVGDVTKGDDVVCIVLEAMKMEITATVDGVITELVN 150  
QY 108 ERDAVQGGQGLIKI 121  
Db 151 NEDVVEFGQPLFRV 164

RESULT 39  
5252466-5  
; Patent No. 5252466  
; APPLICANT: CROGAN, JOHN E.  
; TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN  
; VIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND  
; PURIFYING THEM  
; NUMBER OF SEQUENCES: 24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/525,568  
; FILING DATE: 18-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 354,266  
; FILING DATE: 19-MAY-1989  
; SEQ ID NO:5  
; LENGTH: 67  
5252466-5

Query Match 22.3%; Score 137; DB 6; Length 67;  
Best Local Similarity 50.0%; Pred. No. 1.7e-07;  
Matches 29; Conservative 10; Mismatches 19; Indels 0; Gaps 0;  
QY 58 APLAGTVSKILVKEGDTVKAGOTVLVLEAMKMETEINAPTDGKVKVVKERDAVGG 115  
Db 2 APVVGLEVVKLVKDGKVBQGPVLVLEAMKMEHVVKAPANGYVSGLEIKVQSVQDG 59

RESULT 40  
US-08-611-107-4  
; Sequence 4, Application US/08611107  
; Patent No. 5801233  
; GENERAL INFORMATION:

APPLICANT: Haselkorn, Robert  
APPLICANT: Gornicki, Piotr  
TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODING  
TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE AND USES  
TITLE OF INVENTION: THEREFOR  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/611,107  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US SN 07/956,700  
FILING DATE: 02-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US PCT/US93/09340  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US SN 08/422,560  
FILING DATE: 14-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: ARCD:221  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 158 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-611-107-4

Query Match 22.2%; Score 136.5; DB 1; Length 158;  
Best Local Similarity 35.5%; Pred. No. 5.6e-07;  
Matches 33; Conservative 16; Mismatches 35; Indels 9; Gaps 2;

Qy	38	APAPAGGAGAGKAGEG--EIPAPLAGTVSKI-----LVKEGDTVKAGQTVLVLEAMK 88
Db	63	APTPAAPPPAGPLGGEKELEITAPWVGTFYPAPAPEPPFVNVGDRIQVGQTVLCILEAMK 122
Qy	89	METEINAPTDGKVEKVLVKERDAVGGQGLIKI 121
Db	123	LMNELESEVTGVEVVEILLVQNGEPVEFNPFLRL 155

Search completed: March 3, 2004, 10:32:34  
Job time : 22.3333 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 3, 2004, 10:23:49 ; Search time 36.4583 Seconds  
(without alignments)  
542.491 Million cell updates/sec

Title: US-09-987-485a-2

Perfect score: 342

Sequence: 1 EGEIPAPLAGTVSKILKEG.....XVLVKERDAVGGGGLIKIG 70

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	342	100.0	70	6	ABG72299 Escherich
2	342	100.0	122	6	ABG72298 Escherich
3	342	100.0	123	6	AAR28177 1.3S poly
4	342	100.0	126	6	AAY84002 Amino aci
5	342	100.0	194	6	AAY78908 Outer sur
6	342	100.0	253	6	Aaw11886 Hantaviru
7	342	100.0	256	6	Aay84001 Amino aci
8	342	100.0	266	3	AAY84003
9	263	76.9	125	3	AAU51122 Propionib
10	263	76.9	125	6	ABM47641 Propionib
11	195	57.0	148	4	AAB96610 Putative
12	174	50.9	1148	6	ABU18942 Protein e
13	172	50.3	143	6	ABU21035 Protein e
14	167	48.8	1144	6	ABU24164 Protein e
15	166	48.5	596	6	ABU33366 Protein e
16	165	48.2	588	6	ABU32216 Protein e
17	164	48.0	597	6	ABU49155 Protein e
18	163	47.7	599	6	ABU26544 Protein e
19	160	46.8	602	6	ABU41674 Protein e
20	159	46.5	602	6	ABU39826 Protein e
21	158.5	46.3	1157	5	AAU98050 Coryneb
22	158	46.2	100	2	AAR42120 Oxalaceta
23	158	46.2	607	6	ABU15742 Protein e
24	157	45.9	1146	5	ABB47612 Listeria
25	157	45.9	1146	6	ABU32564 Protein e

26	155.5	45.5	272	4	AAB79298 Coryneb
27	155.5	45.5	272	4	AAB79299 Coryneb
28	155.5	45.5	1139	4	AAB83180 Coryneb
29	155.5	45.5	1140	2	AAG93971 C. glutam
30	155.5	45.5	1140	4	AAB67129 Coryneb
31	155.5	45.5	1140	4	AAG90511 C glutami
32	155.5	45.5	1140	4	AAG93249 C glutami
33	155.5	45.5	1140	5	AAG25601 Coryneb
34	155.5	45.5	1140	5	AAU98053 Coryneb
35	155.5	45.5	1140	7	ABU10426 Coryneb
36	155.5	45.5	1141	3	ABU01436 Pyruvate
37	155.5	45.5	1141	6	ABU25961 Protein e
38	153	44.7	1144	6	ABU24853 Protein e
39	151.5	44.3	1140	5	AAU98052 Coryneb
40	151	44.2	166	5	ABP28014 Streptoco
41	151	44.2	166	6	ABU46782 Protein e
42	151	44.2	1142	6	ABU30018 Protein e
43	150	43.9	190	7	ADC96093 E. faeciu
44	150	43.9	1143	6	ABU24993 Protein e
45	148	43.3	162	6	ABU44260 Protein e

ALIGNMENTS

RESULT 1  
ABG72299  
ID ABG72299 standard; protein; 70 AA.

XX  
AC ABG72299;  
XX  
DT 21-MAR-2003 (first entry)  
XX  
DE Escherichia coli truncated PSTCD protein.

XX Polypeptide labelling; biotinylation-competent fusion partner;  
KW biotin acceptor peptide; BAP; virus; avidin; cell surface protein;  
KW biotin ligase; BirA; drug therapy; gene therapy targeting;  
KW biotin labelled protein; P. shermanii transcarboxylase domain;  
KW truncated PSTCD; mutant; muten.

XX Escherichia coli.  
OS Synthetic.

XX US2002142355-A1.

XX 03-OCT-2002.

XX 14-NOV-2001; 2001US-00987485.

XX 14-NOV-2000; 2000US-0247965P.

XX (BAYU ) BAYLOR COLLEGE MEDICINE.

XX Barry MA, Parrott MB;

XX WPI; 2003-165810/16.

XX Novel fusion protein useful for targeting desired protein to cell in culture or in the body of subject, comprises biotinylation-competent protein/peptide, or biotin acceptor peptide (BAP), and desired polypeptide.

XX Claim 4; Fig 1; 13pp; English.

XX The present invention relates to methods for labelling polypeptides in mammalian cells with biotin. The methods involve expressing the protein joined to a biotinylation-competent fusion partner, or a biotin acceptor peptide (BAP). The fusion protein is useful for targeting a protein of interest which is on the surface of a virus, to a cell in culture, in the body of a subject. The method involves binding avidin to the surface of the cell, biotinylation of the fusion protein, where the protein of interest is joined to the biotinylation-competent protein or peptide, and

CC administering the biotinylated protein to either the medium surrounding  
 CC the cell in culture or to the subject. The protein of interest is used to  
 CC target the virus to the cell. A polynucleotide vector for expressing the  
 CC protein comprises a coding region consisting of nucleotides encoding a  
 CC fusion protein such as biotin ligase (e.g. BirA) directly linked to a  
 CC leader sequence (e.g. Igkappa secretory leader) is useful for  
 CC biotinylating a polypeptide of interest secreted by a mammalian host  
 CC cell. The fusion protein of the invention is useful for drug and gene  
 CC therapy targeting. The biotin labelled proteins are useful for delivering  
 CC nucleic acids to cell in vivo. The method is useful for rapidly purifying  
 CC a virus, for attaching other compounds to the virus, for modifying the  
 CC virus's ability to transduce cells in vivo and ex vivo, and for directing  
 CC the virus to specific avidin-tagged sites in a patient's body. The  
 CC present sequence represents Escherichia coli truncated PSTCD (P.  
 CC shermanii transcarboxylase domain) protein. Truncated PSTCD can be used  
 CC in a fusion protein of the invention

XX Sequence 70 AA;

Query Match 100.0%; Score 342; DB 6; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-34;  
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTQSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVKVLYKRDVAV 60  
 DB 1 EGEIPAPLAGTQSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVKVLYKRDVAV 60  
 QY 61 QGGQGLIKIG 70  
 DB 61 QGGQGLIKIG 70

RESULT 2

ABG72298  
 ID ABG72298 standard; protein; 122 AA.

AC ABG72298;

DT 21-MAR-2003 (first entry)

XX Escherichia coli full-length PSTCD protein.

XX Polypeptide labelling; biotinylation-competent fusion partner;  
 KW biotin acceptor peptide; BAP; virus; avidin; cell surface protein;  
 KW biotin ligase; BirA; drug therapy; Gene therapy targeting;  
 KW biotin labelled protein; P. shermanii transcarboxylase domain; PSTCD.

XX Escherichia coli.

XX US2002142355-A1.

XX 03-OCT-2002.

XX 14-NOV-2001; 2001US-00987485.

XX 14-NOV-2000; 2000US-0247965P.

XX (BAYU ) BAYLOR COLLEGE MEDICINE.

XX Barry MA; Parrott MB;

XX WPI; 2003-165810/16.

XX Novel fusion protein useful for targeting desired protein to cell in  
 PT culture or in the body of subject, comprises biotinylation-competent  
 PT protein/peptide, or biotin acceptor peptide (BAP), and desired  
 PT polypeptide.

XX Claim 2; Fig 1; 13pp; English.

XX The present invention relates to methods for labelling polypeptides in  
 CC mammalian cells with biotin. The methods involve expressing the protein  
 CC joined to a biotinylation-competent fusion partner, or a biotin acceptor

CC peptide (BAP). The fusion protein is useful for targeting a protein of  
 CC interest which is on the surface of a virus, to a cell in culture, in the  
 CC body of a subject. The method involves binding avidin to the surface of  
 CC the cell, biotinylation of the fusion protein, where the protein of  
 CC interest is joined to the biotinylation-competent protein or peptide, and  
 CC administering the biotinylated protein to either the medium surrounding  
 CC the cell in culture or to the subject. The protein of interest is used to  
 CC target the virus to the cell. A polynucleotide vector for expressing the  
 CC protein comprises a coding region consisting of nucleotides encoding a  
 CC fusion protein such as biotin ligase (e.g. BirA) directly linked to a  
 CC leader sequence (e.g. Igkappa secretory leader) is useful for  
 CC biotinylating a polypeptide of interest secreted by a mammalian host  
 CC cell. The fusion protein of the invention is useful for drug and gene  
 CC therapy targeting. The biotin labelled proteins are useful for delivering  
 CC nucleic acids to cell in vivo. The method is useful for rapidly purifying  
 CC a virus, for attaching other compounds to the virus, for modifying the  
 CC virus's ability to transduce cells in vivo and ex vivo, and for directing  
 CC the virus to specific avidin-tagged sites in a patient's body. The  
 CC present sequence represents Escherichia coli full-length PSTCD (P.  
 CC shermanii transcarboxylase domain) protein. PSTCD can be used in a fusion  
 CC protein of the invention

XX Sequence 122 AA;

Query Match 100.0%; Score 342; DB 6; Length 122;

Best Local Similarity 100.0%; Pred. No. 7.2e-34;

Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTQSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVKVLYKRDVAV 60  
 DB 53 EGEIPAPLAGTQSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVKVLYKRDVAV 112

QY 61 QGGQGLIKIG 70

DB 113 QGGQGLIKIG 122

RESULT 3

AAR28177

ID AAR28177 standard; protein; 123 AA.

AC AAR28177;

XX 24-OCT-2003 (revised)

XX 25-MAR-2003 (revised)

DT 18-MAR-1993 (first entry)

XX 1.3S polypeptide of Propionibacterium shermanii.

XX avidin-binding; biotin; protein purification; affinity chromatography.

XX Propionibacterium freudenreichii subsp. shermanii.

XX Key Location/Qualifiers

XX Region 58..100

XX /label= biotin-binding\_recognition\_sequence

XX BP511747-A1.

XX 04-NOV-1992.

XX 07-APR-1992; 92EP-00303067.

XX 19-APR-1991; 91US-00687819.

XX (ROHM ) ROHM & HAAS CO.

XX Cress DE, Haase FC;

XX WPI; 1992-367575/45.

XX N-PSDB; AAQ29975.

XX Hybrid polypeptide - contains a polypeptide fused to an avidin binding

PT polypeptide contg. a biotin attachment domain.

PS Claim 6; Page 23; 40pp; English.

XX The P. shermanii 1.3S polypeptide is a preferred avidin-binding  
CC polypeptide for inclusion in the recombinant hybrid polypeptide of the  
CC invention. In the hybrid, a polypeptide of interest is fused to the C-  
CC terminus of the avidin-binding polypeptide. The hybrid polypeptide can  
CC then be recovered in a single chromatographic step using avidin monomer  
CC affinity chromatography. (Updated on 25-MAR-2003 to correct PN field.)  
CC (Updated on 24-OCT-2003 to standardise OS field)

XX Sequence 123 AA;

Query Match 100.0%; Score 342; DB 2; Length 123;

Best Local Similarity 100.0%; Pred. No. 7.2e-34;

Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAV 60

Db 54 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAV 113

QY 61 QGGQGLIKIG 70

Db 114 QGGQGLIKIG 123

#### RESULT 4

AAAY84002

ID AAY84002 standard; protein; 126 AA.

AC AAY84002;

DT 03-JUL-2000 (first entry)

XX Amino acid sequence of a T. pallidum protein.

XX PinPoint vector; fusion protein antigen; membrane antigen; syphilis.

XX Treponema pallidum.

PN EP985931-A2. ✓

XX 15-MAR-2000.

PD 12-AUG-1999; 92EP-00115877.

PF 04-SEP-1998; 98US-00148920.

PR (BECT ) BECTON DICKINSON & CO.

XX Mullenix MC, Deutsch J;

XX WPI; 2000-226057/20.

DR N-PSDB; AAZ9247.

XX Immunassay for anti-Treponema pallidum antibodies, used for diagnosis of

PT syphilis using a fusion protein of membrane antigen with peptide sequence

PT that can be biotinylated in vivo.

XX Disclosure; Page 12-13; 16pp; English.

XX The present sequence represents a Treponema pallidum protein, which is  
CC used to produce a fusion protein antigen for use in the method of the  
CC invention. The specification describes a method for detecting antibodies  
CC against Treponema pallidum. The antibodies are detected in a sample by  
CC reaction with a fusion protein antigen, present in the mixture in  
CC limiting concentration. The fusion protein antigen comprises a Treponema  
CC pallidum membrane antigen. The method is used for diagnosis of syphilis

XX Sequence 126 AA;

Query Match 100.0%; Score 342; DB 3; Length 126;

Best Local Similarity 100.0%; Pred. No. 1.3e-33;

Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 7.5e-34;

Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAV 60

Db 53 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLVKERDAV 112

QY 61 QGGQGLIKIG 70

Db 113 QGGQGLIKIG,122

#### RESULT 5

AAAY78908

ID AAY78908 standard; protein; 194 AA.

XX AAY78908;

DT 19-MAY-2000 (first entry)

XX Outer surface protein C (OspC) DraI fragment amino acid sequence.

XX Outer surface protein C; OspC; immunological epitope; Lyme disease;

XX vaccine; prevention; Borrelia infection; diagnose.

OS Borrelia burgdorferi.

XX WO200006745-A1.

XX 10-FEB-2000.

XX 30-JUL-1999; 99WO-US017270.

XX 31-JUL-1998; 98US-0094955P.

XX (GUND-) GUNDERSEN LUTHERAN MEDICAL FOUND INC.

XX Callister SN, Lovrich SD, Schell RF, Jobe DA;

XX WPI; 2000-195305/17.

XX N-PSDB; AAZ92216.

XX New immunogenic polypeptides useful as a vaccine against Lyme disease and

XX for treating and detecting borrelia infection in mammals consists an

XX epitope of Borrelia burgdorferi OspC fragment.

XX Claim 3; Fig 4; 51pp; English.

XX This sequence represents the Borrelia burgdorferi outer surface protein C  
(OspC) DraI fragment amino acid sequence. The polypeptide contains an  
CC immunological epitope used in the invention. Large amounts of OspC are  
CC rapidly synthesised by B. burgdorferi shortly after attachment of  
CC infected ticks to mammalian hosts. The OspC protein sequence is used to  
CC diagnose B. Borrelia infection in mammals. The OspC nucleotide sequence  
CC is used to prevent (via vaccination), treat or detect Borrelia  
CC (especially B. burgdorferi) infections, i.e. Lyme disease, in mammals  
CC including humans. The OspC nucleotide sequence provides a superior  
CC diagnostic antigen that detects early Lyme disease infection, predicts  
CC successful eradication or the organism from the host, and discriminates  
CC between individuals with Lyme disease and individuals who have been  
CC vaccinated with an OspA Lyme disease vaccine. Detection of anti-OspC  
CC borrelia antibodies advantageously gives an early diagnosis which  
CC anti-OspA and anti-OspB borrelia antibodies cannot do. Unlike  
CC vaccination with OspA, vaccination with OspC results in clearance of  
CC spirochetes and resolution of symptoms even if administered after  
CC infection with B. burgdorferi

XX Sequence 194 AA;

Query Match 100.0%; Score 342; DB 3; Length 194;

Best Local Similarity 100.0%; Pred. No. 1.3e-33;

Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKGAGTVLVLEAMKMETEINAPTQKVEKVLVKERDAV 60  
Db 53 EGEIPAPLAGTVSKILVKEGDTVKGAGTVLVLEAMKMETEINAPTQKVEKVLVKERDAV 112  
QY 61 QGGQGLIKIG 70  
Db 113 QGGQGLIKIG 122

RESULT 6  
AAW11886  
ID AAW11886 standard; protein; 253 AA.

XX AC AAW11886;

XX DT 21-APR-1997 (first entry)

XX DE Hantavirus nuclear protein sequence.

XX KW Hantavirus nuclear protein; antigen; monoclonal antibody; diagnosis;  
XX KW specificity.

XX OS Hantavirus.

XX PN JPO8325291-A.

XX PD 10-DEC-1996.

XX PF 30-MAY-1995; 95JP-00132460.

XX PR 30-MAY-1995; 95JP-00132460.

XX PA (ARIK/) ARIKAWA J.

XX PA (HASH/) HASHIMOTO N.

XX PA (ATAT-) A & T KK.

XX DR WPI; 1997-083468/08.

XX PT Hantavirus antigen protein and monoclonal antibody - used in the  
XX PT diagnosis and treatment of hantavirus infection.

XX PS Example 1; Page 17; 18pp; Japanese.

XX CC The sequences given in AAW11872-86 represent Hantavirus nuclear proteins.  
XX CC The N-terminal regions of these proteins may be used as antigens to raise  
XX CC anti-hantavirus monoclonal antibodies. These antibodies are useful in  
XX CC diagnosis of hantavirus infection due to their specificity to Hantavirus  
XX SQ Sequence 253 AA;

Query Match 100.0%; Score 342; DB 2; Length 253;  
Best Local Similarity 100.0%; Pred. No. 1.9e-33;  
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKGAGTVLVLEAMKMETEINAPTQKVEKVLVKERDAV 60  
Db 53 EGEIPAPLAGTVSKILVKEGDTVKGAGTVLVLEAMKMETEINAPTQKVEKVLVKERDAV 112

QY 61 QGGQGLIKIG 70

Db 113 QGGQGLIKIG 122

RESULT 7

AAW84001  
ID AAW84001 standard; protein; 256 AA.

XX AC AAW84001;

XX DT 03-JUL-2000 (first entry)

XX DE Amino acid sequence of a T. pallidum fusion protein antigen.

XX XX

PinPoint vector; fusion protein antigen; membrane antigen; syphilis.  
Synthetic.  
Treponema pallidum.

EP985931-A2.

15-MAR-2000.

12-AUG-1999; 99EP-00115877.

04-SEP-1998; 98US-00148920.

(BECT ) BECTON DICKINSON & CO.

Mullenix MC, Deutsch J;

WPI; 2000-226057/20.

N-PSDB; AA299246.

Immunosay for anti-Treponema pallidum antibodies, used for diagnosis of  
syphilis using a fusion protein of membrane antigen with peptide sequence  
that can be biotinylated in vivo.

Claim 9; Page 10-11; 16pp; English.

The present sequence represents a Treponema pallidum fusion protein  
antigen. The protein is used in the method of the invention. The  
specification describes a method for detecting antibodies against  
Treponema pallidum. The antibodies are detected in a sample by reaction  
with a fusion protein antigen, present in the mixture in limiting  
concentration. The fusion protein antigen comprises a Treponema pallidum  
membrane antigen. The method is used for diagnosis of syphilis

Sequence 256 AA;

Query Match 100.0%; Score 342; DB 3; Length 256;  
Best Local Similarity 100.0%; Pred. No. 1.9e-33;  
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKGAGTVLVLEAMKMETEINAPTQKVEKVLVKERDAV 60  
Db 53 EGEIPAPLAGTVSKILVKEGDTVKGAGTVLVLEAMKMETEINAPTQKVEKVLVKERDAV 112

QY 61 QGGQGLIKIG 70

Db 113 QGGQGLIKIG 122

RESULT 8

AAW84003

ID AAW84003 standard; protein; 266 AA.

XX AC AAW84003;

XX DT 03-JUL-2000 (first entry)

XX DE Amino acid sequence of a T. pallidum membrane protein antigen.

XX KW PinPoint vector; fusion protein antigen; membrane antigen; syphilis.

XX OS Treponema pallidum.

XX PN EP985931-A2.

XX PD 15-MAR-2000.

XX PF 12-AUG-1999; 99EP-00115877.

XX PR 04-SEP-1998; 98US-00148920.

XX PA (BECT ) BECTON DICKINSON & CO.

XX XX

KW

XX

OS

XX

PN

XX

PD

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PF

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PR

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PA

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PI

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DR

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PT

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PS

XX

CC

XX

CC

XX

CC

XX

CC

XX

CC

XX

CC

XX

SQ

PI Mullenix MC, Deutsch J;  
 XX WPI: 2000-226057/20.  
 DR N-PSDB; AA299248.  
 XX  
 PT Immunoassay for anti-Treponema pallidum antibodies, used for diagnosis of  
 PT syphilis using a fusion protein of membrane antigen with peptide sequence  
 PT that can be biotinylated in vivo.  
 XX  
 PS Claim 9; Page 14-15; 16pp; English.  
 XX  
 CC The present sequence represents a Treponema pallidum membrane protein  
 CC antigen, which is used to produce a fusion protein antigen for use in the  
 CC method of the invention. The specification describes a method for  
 CC detecting antibodies against Treponema pallidum. The antibodies are  
 CC detected in a sample by reaction with a fusion protein antigen, present  
 CC in the mixture in limiting concentration. The fusion protein antigen  
 CC comprises a Treponema pallidum membrane antigen. The method is used for  
 CC diagnosis of syphilis  
 XX  
 SQ Sequence 266 AA;  
 Query Match 100.0%; Score 342; DB 3; Length 266;  
 Best Local Similarity 100.0%; Pred. No. 2e-33;  
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGEIPAPLAGTYSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVLVXERDAV 60  
 DB 53 EGEIPAPLAGTYSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVLVXERDAV 112  
 QY 61 QGGQGLIKIG 70  
 DB 113 QGGQGLIKIG 122  
 RESULT 9  
 AAUS1122  
 ID AAUS1122 standard; protein; 125 AA.  
 AC AAUS1122;  
 XX  
 DT 27-FEB-2002 (first entry)  
 DE  
 DE Propionibacterium acnes immunogenic protein #12018.  
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;  
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
 KW dermatological; osteopathic; neuroprotectant.  
 XX  
 OS Propionibacterium acnes.  
 PN WO200181581-A2.  
 XX  
 PD 01-NOV-2001.  
 XX  
 PF 20-APR-2001; 2001WO-US012865.  
 XX  
 PR 21-APR-2000; 2000US-0199047P.  
 PR 02-JUN-2000; 2000US-0208841P.  
 PR 07-JUL-2000; 2000US-0216747P.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;  
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;  
 XX  
 DR WPI: 2001-616774/71.  
 DR N-PSDB; AAS59550.  
 XX  
 XX Propionibacterium acnes polypeptides and nucleic acids useful for  
 PT vaccinating against and diagnosing infections, especially useful for  
 PT treating acne vulgaris.

XX  
 PS Claim 6; SEQ ID NO 12317; 1069pp; English.  
 XX  
 CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic  
 CC polypeptides. The proteins and their associated DNA sequences are used in  
 CC the treatment, prevention and diagnosis of medical conditions caused by  
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,  
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.  
 CC P. acnes is also involved in infections of bone, joints and the central  
 CC nervous system, however it is particularly involved in the inflammatory  
 CC lesions associated with acne vulgaris. A method for detecting the  
 CC presence or absence of P. acnes in a patient comprises contacting a  
 CC sample with a binding agent that binds to the proteins of the invention  
 CC and determining the amount of bound protein in the sample. The  
 CC polypeptides may be used as antigens in the production of antibodies  
 CC specific for P. acnes proteins. These antibodies can be used to  
 CC downregulate expression and activity of P. acnes polypeptides and  
 CC therefore treat P. acnes infections. The antibodies may also be used as  
 CC diagnostic agents for determining P. acnes presence, for example, by  
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for  
 CC this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 125 AA;  
 Query Match 76.9%; Score 263; DB 4; Length 125;  
 Best Local Similarity 74.3%; Pred. No. 3.5e-24;  
 Matches 52; Conservative 7; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 EGEIPAPLAGTYSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVLVXERDAV 60  
 DB 56 EGEVPAPLAGTVAKILVAEGDAVKAGQVLLTLEAMKMETEINAPADGTVKGLVAVGDAV 115  
 QY 61 QGGQGLIKIG 70  
 DB 116 QGGQGLVAG 125  
 RESULT 10  
 ABM47641  
 ID ABM47641 standard; protein; 125 AA.  
 XX  
 AC ABM47641;  
 XX  
 DT 20-OCT-2003 (first entry)  
 XX  
 DE Propionibacterium acnes immunogenic polypeptide #12317.  
 XX  
 KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;  
 KW immunostimulant; immune response; vaccine; immunogenic.  
 XX  
 OS Propionibacterium acnes.  
 XX  
 PN WO2003033515-A1.  
 XX  
 PD 24-APR-2003.  
 XX  
 PF 11-OCT-2002; 2002WO-US032727.  
 XX  
 PR 15-OCT-2001; 2001US-00978825.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;  
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;  
 PI Barth B, Vallie-Douglass J;  
 XX  
 DR WPI: 2003-381789/36.  
 DR N-PSDB; ACF64479.  
 XX  
 XX New Propionibacterium acnes polypeptides and polynucleotides encoding the  
 PT polypeptide, useful for diagnosing and preventing or treating acne vulgaris,

PT or for stimulating an immune response specific for a P. acnes protein.  
XX Claim 6; SEQ ID NO 12317; 1481pp; English.  
PS  
XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)  
CC encoding a Propionibacterium acnes protein. The invention also relates to  
CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to  
CC immunogenic fragments of P. acnes polypeptides. The invention  
CC additionally encompasses expression vectors and host cells comprising a  
CC polynucleotide of the invention; antibodies against polypeptides of the  
CC invention; fusion proteins comprising a polypeptide of the invention; a  
CC method for stimulating an immune response specific for a P. acnes  
CC polypeptide and an isolated T cell population comprising T cells prepared  
CC via this method; a vaccine composition (comprising P. acnes polypeptides,  
CC polynucleotides, antibodies, fusion proteins, T cell populations, or  
CC antigen-presenting cells that express the polypeptide); a method and kit  
CC for detecting or determining the presence or absence of P. acnes in a  
CC patient; and a method for inhibiting the development of P. acnes in a  
CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion  
CC proteins, T cell populations or antigen-presenting cells that express the  
CC polypeptides are useful for diagnosing, preventing or treating acne  
CC vulgaris, or for stimulating an immune response specific for a P. acnes  
CC protein. The polynucleotides can also be used as probes or primers for  
CC nucleic acid hybridisation. The vaccine composition is useful for the  
CC stimulation of an immune response against P. acnes, or for treating acne,  
CC and the kit is useful for performing a diagnostic assay. The present  
CC sequence represents a specifically claimed P. acnes polypeptide which is  
CC thought to contain an immunogenic region. Note: The sequence data for  
CC this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 125 AA;

Query Match 76.9%; Score 263; DB 6; Length 125;  
Best Local Similarity 74.3%; Pred. No. 3.5e-24;  
Matches 52; Conservative 7; Mismatches 11; Indels 0; Gaps 0;  
QY 1 EGEIPAPLAGTYSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60  
DB 56 EGEVPAPLAGTVAKILVAGSDAVKAGQVLLTLEAMKMETEINAPADGTGKILVAGDAV 115  
QY 61 QGGQGLIKIG 70  
DB 116 QGGQGLVALG 125

RESULT 11  
AAB96610  
ID AAB96610 standard; protein; 148 AA.  
XX  
AC AAB96610;  
XX  
DT 29-OCT-2001 (first entry)  
XX  
DE Putative biotin carboxylase carrier protein of acetyl-CoA carboxylase.  
XX  
KW Hyperthermophilic archaeon; hyperthermophilic protein.  
XX  
OS Pyrococcus abyssi.  
XX  
PN FR2792651-A1.  
XX  
PD 27-OCT-2000.  
XX  
PF 21-APR-1999; 99FR-00005034.  
XX  
PR 21-APR-1999; 99FR-00005034.  
XX  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
XX (IFRE-) IFREMER INST FR RECH EXPL MER.  
PI Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;

PI Querellou J, Weissenbach J, Saurin W, Heilig R;  
XX WPI; 2001-126236/14.  
DR  
XX New nucleotide sequences isolated from Pyrococcus abyssi encode proteins  
PT useful in industry.  
XX  
XX Claim 7; Page 1349; 1657pp; French.  
XX  
CC The present invention relates to the genomic sequence of Pyrococcus  
CC abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is  
CC a hyperthermophilic archaeon, which is isolated from deep-sea  
CC hydrothermal vents. The present sequence is one such P. abyssi protein.  
CC The proteins of the present invention have various potential industrial  
CC uses, since the proteins are stable at very high temperatures, some up to  
CC 110 degrees centigrade. Note: This patent is in the same patent family as  
CC WO200065062, which contains additional sequences as shown in AAB99132-  
CC AAB99143, AAH75903-AAH75920 and AAG66436  
XX  
SQ Sequence 148 AA;

Query Match 57.0%; Score 195; DB 4; Length 148;  
Best Local Similarity 58.8%; Pred. No. 9.3e-16;  
Matches 41; Conservative 10; Mismatches 19; Indels 0; Gaps 0;  
QY 1 EGEIPAPLAGTYSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60  
DB 79 ENVVTFAPMGKVLKILVQSGQVKGQGLLLEAMKMETEINAPRDSGVVVKRILVKEGDAV 138  
QY 61 QGGQGLIKIG 70  
DB 139 DTGTPLIELG 148

RESULT 12  
ABU18942  
ID ABU18942 standard; protein; 1148 AA.  
XX  
AC ABU18942;  
XX  
XX 19-JUN-2003 (first entry)  
DT  
DE Protein encoded by Prokaryotic essential gene #4469.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Bacillus anthracis.  
XX  
PN WC200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA22812.  
XX  
XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 46866; 1766pp; English.



XX The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 1148 AA;

Query Match 50.9%; Score 174; DB 6; Length 1148;  
 Best Local Similarity 53.0%; Pred. No. 5e-12;  
 Matches 35; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 4 IPAPLACTVSKILVKEGDTVKAGQTVLVLEAMKMEINAPTQKVEKVLKRDVQGG 63  
 Db 1081 ISATMPGTIVIKVVVKEGDEVKGDMAITEAMKMETTVQAPFNGKVKVYVNDGDAIQTG 1140  
 QY 64 QGLIKI 69  
 Db 1141 DLLIEL 1146

RESULT 13  
 ABU21035  
 ID ABU21035 standard; protein; 143 AA.  
 XX  
 AC ABU21035;  
 XX  
 DT 19-JUN-2003 (first entry)  
 XX  
 DE Protein encoded by Prokaryotic essential gene #6562.  
 XX  
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 XX  
 OS Bacteroides fragilis.  
 XX  
 PN WO200277183-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 21-MAR-2002; 2002WO-US009107.  
 XX  
 PR 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00948993.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.  
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
 PI Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;  
 XX WPI; 2003-029926/02.  
 DR N-PSDB; ACA24905.  
 XX  
 PT New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.  
 XX Claim 25; SEQ ID NO 48959; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 143 AA;

Query Match 50.3%; Score 172; DB 6; Length 143;  
 Best Local Similarity 53.0%; Pred. No. 5.8e-13;  
 Matches 35; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

QY 4 IPAPLACTVSKILVKEGDTVKAGQTVLVLEAMKMEINAPTQKVEKVLKRDVQGG 63  
 Db 77 VKSPFGVILDIKVKEGDTVKRGQTIIILEAMKMEINANKDKGVAEIKVNGKDSVLEG 136  
 QY 64 QGLIKI 69  
 Db 137 TDLVII 142

RESULT 14  
 ABU24164  
 ID ABU24164 standard; protein; 1144 AA.  
 XX  
 AC ABU24164;  
 XX  
 DT 19-JUN-2003 (first entry)  
 XX  
 DE Protein encoded by Prokaryotic essential gene #9691.  
 XX  
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.



ftp.wipo.int/pub/published\_pct\_sequences  
SQ Sequence 596 AA;

Query Match 48.5%; Score 166; DB 6; Length 596;  
Best Local Similarity 51.5%; Pred. No. 2e-11;  
Matches 35; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 2 GEIPAPLAGTISKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLKRDVAQ 61  
Db 526 GDTVAIPGSIATIHVSVDGKAGQAVLVIEAMKMETEIKAPANGVVAELICQKDKVT 585  
QY 62 GQGLIKI 69  
Db 586 PGQVLIRV 593

RESULT 16  
ABU32216  
ID ABU32216 standard; protein; 598 AA.  
XX  
AC ABU32216;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #17743.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Klebsiella pneumoniae.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA36086.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 60140; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an

organism acts; (9) manufacturing an antibiotic; (10) profiling a  
compound's activity; (11) a culture comprising strains in which the gene  
product is overexpressed or underexpressed; (12) determining the extent  
to which each of the strains is present in a culture or collection of  
strains; or (13) identifying the target of a compound that inhibits the  
proliferation of an organism. The antisense nucleic acids are useful for  
identifying proteins or screening for homologous nucleic acids required  
for cellular proliferation to isolate candidate molecules for rational  
drug discovery programs, or for screening homologous nucleic acids  
required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
*K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
the target prokaryotic essential genes. Note: The sequence data for this  
patent did not form part of the printed specification, but was obtained  
in electronic format directly from WIPO at  
ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 588 AA;

Query Match 48.2%; Score 165; DB 6; Length 588;  
Best Local Similarity 53.0%; Pred. No. 2.6e-11;  
Matches 35; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

QY 4 IPAPLAGTISKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLKRDVAQGG 63  
Db 522 VTAPLAGTINKVLASEGQTVAAAGEVLLILEAMKMETEIRAAQAGTVRGIAVKAGDAVAVG 581  
QY 64 QGLIKI 69  
Db 582 DTLMTL 587

RESULT 17  
ABU49155  
ID ABU49155 standard; protein; 597 AA.  
XX  
AC ABU49155;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #34682.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Vibrio cholerae.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.  
PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI; 2003-029926/02.  
DR N-PSDB; ACA53025.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 77079; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression













PR 08-JUL-1999; 99DE-01031434.  
 PR 08-JUL-1999; 99DE-01031510.  
 PR 08-JUL-1999; 99DE-01031562.  
 PR 08-JUL-1999; 99DE-01031634.  
 PR 09-JUL-1999; 99DE-01032180.  
 PR 09-JUL-1999; 99DE-01032227.  
 PR 09-JUL-1999; 99DE-01032230.  
 PR 09-JUL-1999; 99DE-01032088.  
 PR 14-JUL-1999; 99DE-01032924.  
 PR 14-JUL-1999; 99DE-01032973.  
 PR 14-JUL-1999; 99DE-01033005.  
 PR 27-AUG-1999; 99DE-01040765.  
 PR 31-AUG-1999; 99US-0151572P.  
 PR 03-SEP-1999; 99DE-01042076.  
 PR 03-SEP-1999; 99DE-01042079.  
 PR 03-SEP-1999; 99DE-01042086.  
 PR 03-SEP-1999; 99DE-01042087.  
 PR 03-SEP-1999; 99DE-01042088.  
 PR 03-SEP-1999; 99DE-01042095.  
 PR 03-SEP-1999; 99DE-01042123.  
 PR 03-SEP-1999; 99DE-01042125.

XX (BADI ) BASF AG.

XX Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;

XX WPI; 2001-061975/07.

DR N-PSDB; AAF71415.

XX New isolated Corynebacterium glutamicum nucleic acid encoding a sugar  
 PT metabolism and oxidative phosphorylation protein for production or  
 PT modulation of production of fine chemicals e.g. amino acids,  
 PT carbohydrates or enzymes.

XX Claim 20; Page 307-308; 1245pp; English.

XX AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar  
 CC metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243  
 CC to AAB 79633 which are involved in carbon metabolism and energy  
 CC production. The C. glutamicum SMP gene can be used in vectors (II) for  
 CC expression in host cells and production or modulation of production of  
 CC fine chemicals, such as, an organic acid, a proteinogenic or  
 CC nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a  
 CC nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid,  
 CC a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a  
 CC polyketide, or an enzyme. The presence of (I) or SMP proteins (III)  
 CC encoded by them are used for diagnosing the presence or activity of  
 CC Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells  
 CC containing them are used to map genomes of organisms related to C.  
 CC glutamicum, identify and localise C. glutamicum sequences of interest, in  
 CC evolutionary studies, in determining SMP protein regions required for  
 CC function, in modulating SMP protein activity, in modulating the  
 CC metabolism of sugars, and in modulating high-energy molecule production  
 CC in a cell (i.e. ATP, NADPH)

XX Sequence 272 AA;

Query Match 45.5%; Score 155.5; DB 4; Length 272;  
 Best Local Similarity 44.9%; Pred. No. 1.4e-10;  
 Matches 31; Conservative 14; Mismatches 23; Indels 1; Gaps 1;

QY 1 EGRIPACTGSKILVKGSDTVKAGOTVLVLKAMKMETEINAPTQGVKVLVKERDAV 60  
 Db 204 KGHVADPAGVVT-VTVAEGDEVKAGDAVAIIAMKWEATITASVDGKIDRVVVPATKV 262

QY 61 QGGQGLIKI 69

Db 263 EGGDLIVV 271

RESULT 27

AAB79299

ID AAB79299 standard; protein; 272 AA.

XX AAB79299;

XX 30-APR-2001 (first entry)

XX Corynebacterium glutamicum SMP protein sequence SEQ ID NO:114.

XX Corynebacterium glutamicum; carbon metabolism and energy production;  
 KW SMP protein; sugar metabolism and oxidative phosphorylation protein;  
 KW fine chemical production; organic acid; proteinogenic amino acid;  
 KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;  
 KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;  
 KW carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;  
 KW diagnosis; Corynebacterium diphtheriae; evolutionary study.

XX Corynebacterium glutamicum.

XX WO200100844-A2.

XX 04-JAN-2001.

XX 23-JUN-2000; 2000WO-IB000943.

XX 25-JUN-1999; 99US-0141031P.

PR 08-JUL-1999; 99DE-01031412.

PR 08-JUL-1999; 99DE-01031413.

PR 08-JUL-1999; 99DE-01031419.

PR 08-JUL-1999; 99DE-01031420.

PR 08-JUL-1999; 99DE-01031424.

PR 08-JUL-1999; 99DE-01031428.

PR 08-JUL-1999; 99DE-01031431.

PR 08-JUL-1999; 99DE-01031433.

PR 08-JUL-1999; 99DE-01031434.

PR 08-JUL-1999; 99DE-01031510.

PR 08-JUL-1999; 99DE-01031562.

PR 08-JUL-1999; 99DE-01031634.

PR 09-JUL-1999; 99DE-01032180.

PR 09-JUL-1999; 99DE-01032227.

PR 09-JUL-1999; 99DE-01032230.

PR 09-JUL-1999; 99US-0143208P.

PR 14-JUL-1999; 99DE-01032924.

PR 14-JUL-1999; 99DE-01032973.

PR 14-JUL-1999; 99DE-01033005.

PR 27-AUG-1999; 99DE-01040765.

PR 31-AUG-1999; 99US-0151572P.

PR 03-SEP-1999; 99DE-01042076.

PR 03-SEP-1999; 99DE-01042079.

PR 03-SEP-1999; 99DE-01042086.

PR 03-SEP-1999; 99DE-01042087.

PR 03-SEP-1999; 99DE-01042088.

PR 03-SEP-1999; 99DE-01042095.

PR 03-SEP-1999; 99DE-01042123.

PR 03-SEP-1999; 99DE-01042125.

XX (BADI ) BASF AG.

XX Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;

XX WPI; 2001-061975/07.

XX N-PSDB; AAF71416.

XX New isolated Corynebacterium glutamicum nucleic acid encoding a sugar  
 PT metabolism and oxidative phosphorylation protein for production or  
 PT modulation of production of fine chemicals e.g. amino acids,  
 PT carbohydrates or enzymes.

XX Claim 20; Page 310-311; 1245pp; English.

XX AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar  
 CC metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243  
 CC to AAB 79633 which are involved in carbon metabolism and energy  
 CC production. The C. glutamicum SMP gene can be used in vectors (II) for  
 CC expression in host cells and production or modulation of production of



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XX      Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW      organic acid synthesis.
XX      Corynebacterium glutamicum.
OS      EP1108790-A2.
XX      20-JUN-2001.
XX      18-DEC-2000; 2000BP-00127688.
XX      16-DEC-1999; 99JP-00377484.
XX      07-APR-2000; 2000JP-00159162.
XX      03-AUG-2000; 2000JP-00280988.
XX      (KYOW ) KYOWA HAKKO KOGYO KK.
XX      Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
XX      Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX      WPI; 2001-376931/40.
XX      N-PSDB; AAH65730.
XX      Novel polynucleotides derived from Coryneform bacteria, for identifying
XX      mutation point of a gene, measuring expression of a gene, analyzing
XX      expression profile or pattern of a gene and identifying homologous gene.
XX      Claim 17; SEQ ID NO 4265; 246pp + Sequence Listing; English.
XX      The present invention provides a number of nucleotide and protein
XX      sequences from the Coryneform bacterium Corynebacterium glutamicum. These
XX      are useful for identifying the mutation point of a gene derived from a
XX      mutant of coryneform bacterium, measuring expression amount and analysing
XX      the expression profile or expression pattern of a gene derived from
XX      Coryneform bacterium, and identifying a homologus of a gene derived from
XX      coryneform bacterium. Coryneform bacteria are useful for producing amino
XX      acids, nucleic acids, vitamins, saccharides and organic acids,
XX      particularly L-lysine. The present sequence is a protein described in the
XX      exemplification of the invention. Note: The sequence data for this patent
XX      did not form part of the printed specification, but was obtained in
XX      electronic format directly from the European Patent Office
XX      SQ      Sequence 1140 AA;
XX      Query Match      45.5%; Score 155.5; DB 4; Length 1140;
XX      Best Local Similarity 44.9%; Pred. No. 9.1e-10;
XX      Matches 31; Conservative 14; Mismatches 23; Indels 1; Gaps 1;
XX      QY      1 EGIIPAPLACTVSKILVKEGDTYKAGTQVLVLEAMKMETINAPTDCGKVKVLYKERDAV 60
XX      DB      1072 KGHVAAPFAGVVT-VTTAEGDEYKAGDAVAIIIEAMKMEATITASVDGKIDRVVVPATKV 1130
XX      QY      61 QGGQGLIKI 69
XX      DB      1131 EGGDLIVVV 1139
XX      RESULT 32
XX      AAG93249
XX      ID      AAG93249 standard; protein; 1140 AA.
XX      AC      AAG93249;
XX      DT      26-SEP-2001 (first entry)
XX      C glutamicum protein fragment mutant P458S.
XX      Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
XX      organic acid synthesis; mutant; mutein.
XX      Corynebacterium glutamicum.
XX      OS      Synthetic.

```



XX Novel mutated, feedback resistant pyruvate carboxylase enzyme  
 PT polypeptide, useful for producing amino acids e.g. L-lysine, L-threonine,  
 PT L-glycine, L-glutamic acid, L-proline and L-methionine and L-isoleucine.  
 XX  
 PS Disclosure; Fig 2; 42pp; English.  
 XX  
 CC The present invention relates to a new mutated, feedback-resistant  
 CC pyruvate carboxylase enzyme. The invention is useful for producing an  
 CC amino acid (e.g. L-lys, L-thr, L-met, L-ile, L-glu, L-arg and L-pro), by  
 CC culturing a host cell in a suitable media and separating the amino acid  
 CC from the medium. The vector of the invention is useful for replacement of  
 CC a wild-type pyruvate carboxylase gene, with a feedback resistant pyruvate  
 CC carboxylase gene, in a Corynebacterium glutamicum, by replacing a genomic  
 CC copy of the wild-type pyruvate carboxylase gene with a selectable marker  
 CC gene through homologous recombination to form a first recombinant  
 CC strain, and replacing the selectable marker gene in the first recombinant  
 CC strain, with feedback resistant pyruvate carboxylase gene through  
 CC homologous recombination to form a second recombinant strain, where the  
 CC homologous recombination in the above steps, occurs between the host cell  
 CC and the vector. The feedback-resistant pyruvate carboxylase enzyme is  
 CC resistant to feedback inhibition from aspartic acid. The present amino  
 CC acid sequence represents the wild-type feedback-resistant pyruvate  
 CC carboxylase enzyme of the invention  
 XX  
 SQ Sequence 1140 AA;  
 Query Match 45.5%; Score 155.5; DB 5; Length 1140;  
 Best Local Similarity 44.9%; Pred. No. 9.1e-10;  
 Matches 31; Conservative 14; Mismatches 23; Indels 1; Gaps 1;  
 QY 1 EGEIPAPLAGTYSKILVKEGTVKAGQTVLVLEAMKMETEINAPTQGVKVKLVKRDVAV 60  
 DB 1072 KGHVAAPFAGVVT-VTVAGDEVKAGDAVAITEAMKMEATITASVDGKIDRVVVPATKV 1130  
 QY 61 QGGQGLIKI 69  
 DB 1131 EGGDLIVVV 1139  
 RESULT 36  
 ABU10426  
 ID ABU10426 standard; protein; 1140 AA.  
 XX  
 AC ABU10426;  
 XX  
 DT 25-AUG-2003 (first entry)  
 XX  
 DE Corynebacterium glutamicum pyruvate carboxylase.  
 KW Pyruvate carboxylase; gene; anaplerotic enzyme; oxaloacetate;  
 KW biosynthesis; growth; lysine production; glutamic acid production;  
 KW industrial fermentation; enzyme.  
 XX  
 OS Corynebacterium glutamicum.  
 XX  
 PN US2003027305-A1.  
 XX  
 PD 06-FEB-2003.  
 XX  
 PF 15-JAN-2002; 2002US-00045072.  
 PR 23-DEC-1998; 98US-00220081.  
 PR 03-OCT-2000; 2000US-00677575.  
 XX  
 PA (ARCH ) ARCHER-DANIELS MIDLAND CO.  
 XX  
 PI Sinskey AJ, Lessard PA, Willis LB;  
 XX  
 XX WPI; 2003-479542/58.  
 DR N-PSDB; ACA62133.  
 XX  
 PT New pyruvate carboxylase from Corynebacterium glutamicum, useful as an

PT anaplerotic enzyme replenishing oxaloacetate consumed for biosynthesis  
 PT during growth, or for lysine or glutamic acid production in industrial  
 XX fermentations.  
 PS Claim 1; Page 16-19; 29pp; English.  
 XX  
 CC The invention describes a new isolated pyruvate carboxylase polypeptide  
 CC having an amino acid sequence at least 95% identical to a sequence  
 CC comprising 1140 amino acids from Corynebacterium glutamicum, or the  
 CC complete amino acid sequence encoded by the cosmid clone deposited with  
 CC the American Type Culture Collection. The polypeptide is useful as an  
 CC anaplerotic enzyme replenishing oxaloacetate consumed for biosynthesis  
 CC during growth. The polypeptide is also useful for lysine or glutamic acid  
 CC production in industrial fermentations. This is the amino acid sequence  
 CC of Corynebacterium glutamicum pyruvate carboxylase  
 XX  
 SQ Sequence 1140 AA;  
 Query Match 45.5%; Score 155.5; DB 7; Length 1140;  
 Best Local Similarity 44.9%; Pred. No. 9.1e-10;  
 Matches 31; Conservative 14; Mismatches 23; Indels 1; Gaps 1;  
 QY 1 EGEIPAPLAGTYSKILVKEGTVKAGQTVLVLEAMKMETEINAPTQGVKVKLVKRDVAV 60  
 DB 1072 KGHVAAPFAGVVT-VTVAGDEVKAGDAVAITEAMKMEATITASVDGKIDRVVVPATKV 1130  
 QY 61 QGGQGLIKI 69  
 DB 1131 EGGDLIVVV 1139  
 RESULT 36  
 AAB01436  
 ID AAB01436 standard; protein; 1141 AA.  
 XX  
 AC AAB01436;  
 XX  
 DT 20-OCT-2000 (first entry)  
 XX  
 DE Pyruvate carboxylase of C. glutamicum.  
 KW Pyruvate carboxylase; expression; amino acid biosynthesis; lysine;  
 KW glutamic acid; oxaloacetate; fermentation; biosynthesis.  
 XX  
 OS Corynebacterium glutamicum.  
 XX  
 PN WO200039305-A1.  
 XX  
 PD 06-JUL-2000.  
 XX  
 PF 23-DEC-1998; 98WO-US027301.  
 XX  
 PR 23-DEC-1998; 98WO-US027301.  
 XX  
 PA (SINS/) SINSKEY A J.  
 PA (LESS/) LESSARD P A.  
 PA (WILL/) WILLIS L B.  
 XX  
 PI Sinskey AJ, Lessard PA, Willis LB;  
 XX  
 XX WPI; 2000-465746/40.  
 DR N-PSDB; AAA47533.  
 XX  
 PT Novel polynucleotides encoding Corynebacterium glutamicum pyruvate  
 PT carboxylase useful for industrial fermentation processes comprises a  
 PT specific nucleotide sequence.  
 XX  
 PS Claim 3; Fig 1; 51pp; English.  
 XX  
 CC The pyruvate carboxylase of Corynebacterium glutamicum can be used for  
 CC producing amino acids, preferably lysine and glutamic acid in industrial  
 CC fermentations and for replenishing oxaloacetate consumed for biosynthesis  
 CC during growth. By incorporating the pyruvate carboxylase gene in

CC expression vectors levels of expression can be 2 - 20 fold higher than in  
 CC Corynebacterium glutamicum  
 XX Sequence 1141 AA;  
 SQ Query Match 45.5%; Score 155.5; DB 3; Length 1141;  
 Best Local Similarity 44.9%; Pred. No. 9.1e-10;  
 Matches 31; Conservative 14; Mismatches 23; Indels 1; Gaps 1;  
 QY 1 EGEIPAPLAGTGVSKILVKEGDTVKAGQTVLVLEAMKMETINAPTQGVKVKLVKRDVAV 60  
 Db 1073 KGVAPAFAGVVT-VTVAEGDEVKAGDAVAIEAMKMEATITASVDGKIDRVVVPAAATKV 1131  
 QY 61 QGGQGLIKI 69  
 Db 1132 EGGDLIVV 1140

RESULT 37  
 ABU25961  
 ID ABU25961 standard; protein; 1141 AA.  
 XX  
 AC ABU25961:  
 DT 19-JUN-2003 (first entry)  
 XX Protein encoded by Prokaryotic essential gene #11488.  
 DE Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 XX  
 KW Corynebacterium diphtheriae.  
 OS  
 PN WO200277183-A2.  
 XX  
 XX 03-OCT-2002.  
 XX 21-MAR-2002; 2002WO-US009107.  
 XX 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00948993.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.  
 XX  
 XX (ELIT-) ELITRA PHARM INC.  
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlseen KL, Zyskind JW;  
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
 XX WPI; 2003-029926/02.  
 DR N-PSDB; ACA29831.  
 XX New antisense nucleic acids, useful for identifying proteins or screening  
 XX for homologous nucleic acids required for cellular proliferation to  
 XX isolate candidate molecules for rational drug discovery programs.  
 XX Claim 25; SEQ ID NO 53885; 1766pp; English.  
 XX The invention relates to an isolated nucleic acid comprising any one of  
 XX the 6213 antisense sequences given in the specification where expression  
 XX of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies

or a gene on which the test compound that inhibits proliferation of an  
 organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 compound's activity; (11) a culture comprising strains in which the gene  
 product is overexpressed or underexpressed; (12) determining the extent  
 to which each of the strains is present in a culture or collection of  
 strains; or (13) identifying the target of a compound that inhibits the  
 proliferation of an organism. The antisense nucleic acids are useful for  
 identifying proteins or screening for homologous nucleic acids required  
 for cellular proliferation to isolate candidate molecules for rational  
 drug discovery programs, or for screening homologous nucleic acids  
 required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
*K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 the target prokaryotic essential genes. Note: The sequence data for this  
 patent did not form part of the printed specification, but was obtained  
 in electronic format directly from WIPO at  
 ftp.wipo.int/pub/published\_pct\_sequences

XX  
 SQ Sequence 1141 AA;  
 Query Match 45.5%; Score 155.5; DB 6; Length 1141;  
 Best Local Similarity 47.1%; Pred. No. 9.1e-10;  
 Matches 32; Conservative 15; Mismatches 20; Indels 1; Gaps 1;  
 QY 2 GEIPAPLAGTGVSKILVKEGDTVKAGQTVLVLEAMKMETINAPTQGVKVKLVKRDVAV 61  
 Db 1074 KGVAPAFAGVVT-VTIEGATVKAGDPVAVIEAMKMEATISATTDGTVDRVLTQATKVE 1132  
 QY 62 QGGQGLIKI 69  
 Db 1133 EGGDLIVV 1140

RESULT 38  
 ABU24853  
 ID ABU24853 standard; protein; 1144 AA.  
 XX  
 AC ABU24853:  
 XX 19-JUN-2003 (first entry)  
 DT Protein encoded by Prokaryotic essential gene #10380.  
 DE Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 XX  
 KW Clostridium botulinum.  
 OS  
 PN WO200277183-A2.  
 XX  
 XX 03-OCT-2002.  
 XX 21-MAR-2002; 2002WO-US009107.  
 XX 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00948993.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.  
 XX  
 XX (ELIT-) ELITRA PHARM INC.  
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlseen KL, Zyskind JW;  
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
 XX WPI; 2003-029926/02.  
 DR N-PSDB; ACA28723.  
 XX New antisense nucleic acids, useful for identifying proteins or screening  
 XX for homologous nucleic acids required for cellular proliferation to  
 XX isolate candidate molecules for rational drug discovery programs.  
 XX Claim 25; SEQ ID NO 52777; 1766pp; English.  
 XX The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *X. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 CC SQ Sequence 1144 AA;

Query Match 44.7%; Score 153; DB 6; Length 1144;  
 Best Local Similarity 48.5%; Pred. No. 1.8e-09;  
 Matches 32; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

QY 4 IPAPLAGTVSKILVKEGTVVAGQTVLVLEAMKMETETNAPDGVKVKLVKERDAVGG 63  
 DB 1078 IGSSIPGVIVKLVNKGDEIKEGDSLIVLEAMKMETNIVASLSGVGSLVKEGQVKSQ 1137  
 QY 64 QQLIKI 69  
 DB 1138 QLLLEL 1143

RESULT 39  
 AAU98052  
 ID AAU98052 standard; protein; 1140 AA.  
 AC AAU98052;  
 XX  
 XX 27-AUG-2002 (first entry)  
 XX Corynebacterium mutant feedback-resistant pyruvate carboxylase enzyme.  
 XX Feedback-resistant; pyruvate carboxylase; enzyme;  
 KW aspartic acid feedback inhibition resistant; mutant; mutein.  
 XX  
 OS Corynebacterium glutamicum.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 1  
 FT /note= "Wild-type Met substituted by Val"  
 FT Misc-difference 153  
 FT /note= "Wild-type Glu substituted by Asp"  
 FT Misc-difference 182  
 FT /note= "Wild-type Ala substituted by Ser"  
 FT Misc-difference 206  
 FT /note= "Wild-type Ala substituted by Ser"  
 FT Misc-difference 227  
 FT /note= "Wild-type His substituted by Arg"

FT Misc-difference 455  
 FT /note= "Wild-type Ala substituted by Gly"  
 FT Region 1110. .1122  
 FT /note= "Specifically claimed in claim 18"  
 FT Misc-difference 1116  
 FT /note= "Wild-type Asp substituted by Glu"  
 XX  
 XX WO200231158-A2.  
 XX  
 XX 18-APR-2002.  
 XX  
 XX 12-OCT-2001; 2001WO-US031893.  
 XX  
 XX 13-OCT-2000; 2000US-0239913P.  
 XX  
 XX (ARCH ) ARCHER-DANIELS MIDLAND CO.  
 XX  
 XX Hanke PD;  
 XX  
 XX WPI; 2002-463267/49.  
 XX  
 XX Novel mutated, feedback resistant pyruvate carboxylase enzyme  
 XX polypeptide, useful for producing amino acids e.g. L-lysine, L-threonine,  
 XX L-glycine, L-glutamic acid, L-proline and L-methionine and L-isoleucine.  
 XX  
 XX Claim 1; Page: 42pp; English.  
 XX  
 XX The present invention relates to a new mutated, feedback-resistant  
 XX pyruvate carboxylase enzyme. The invention is useful for producing an  
 XX amino acid (e.g. L-lys, L-thr, L-Met, L-Ile, L-Glu, L-Arg and L-Pro), by  
 XX culturing a host cell in a suitable media and separating the amino acid  
 XX from the medium. The vector of the invention is useful for replacement of  
 XX a wild-type pyruvate carboxylase gene, with a feedback resistant pyruvate  
 XX carboxylase gene, in a Corynebacterium glutamicum, by replacing a genomic  
 XX copy of the wild-type pyruvate carboxylase gene with a selectable marker  
 XX gene through homologous recombination to form a first recombinant  
 XX strain, and replacing the selectable marker gene in the first recombinant  
 XX strain, with feedback resistant pyruvate carboxylase gene through  
 XX homologous recombination to form a second recombinant strain, where the  
 XX homologous recombination in the above steps, occurs between the host cell  
 XX and the vector. The feedback-resistant pyruvate carboxylase enzyme is  
 XX resistant to feedback inhibition from aspartic acid. The present amino  
 XX acid sequence represents the mutant feedback-resistant pyruvate  
 XX carboxylase enzyme of the invention. Note: The present sequence is not  
 XX shown in the specification but is derived from the wild-type feedback-  
 XX resistant pyruvate carboxylase enzyme (AAU98053) given in figure 2 of the  
 XX specification

SQ Sequence 1140 AA;

Query Match 44.3%; Score 151.5; DB 5; Length 1140;  
 Best Local Similarity 43.5%; Pred. No. 2.8e-09;  
 Matches 30; Conservative 15; Mismatches 23; Indels 1; Gaps 1;

QY 1 EGETPAPLAGTVSKILVKEGTVVAGQTVLVLEAMKMETETNAPDGVKVKLVKERDAV 60  
 DB 1072 KGHVAAPFAGVVT-VTVAEGDEVKAGDAVAITEAMKMEATITASVEGKIDRVVVPAAATKV 1130  
 QY 61 OGGQGLIKI 69  
 DB 1131 EGGDLIVVV 1139

RESULT 40  
 ABP28014  
 ID ABP28014 standard; protein; 166 AA.  
 XX  
 XX AC ABP28014;  
 XX  
 XX 02-JUL-2002 (first entry)

XX Streptococcus polypeptide SEQ ID NO 5204.  
 DE  
 XX

KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.

XX Streptococcus pyogenes.

XX WO200234771-A2.

XX 02-MAY-2002.

XX 29-OCT-2001; 2001WO-GB004789.

XX 27-OCT-2000; 2000GB-00026333.

PR 24-NOV-2000; 2000GB-00028727.

PR 07-MAR-2001; 2001GB-00005640.

XX (CHIR-) CHIRON SPA.

PA (GENO-) INST GENOMIC RES.

XX Telford J, Masignani V, Margarit Y RosI, Grandi G, Fraser C;

PI Tettelin H;

XX WPI: 2002-352536/38.

DR N-PSDB; ABN68645.

XX New Streptococcus protein for the treatment or prevention of infection or

PT disease caused by Streptococcus bacteria, such as meningitis, and for

PT detecting a compound that binds to the protein.

XX Claim 1; Page 3684; 4525pp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B

CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS

CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in

CC the specification. The proteins have antibacterial and antiinflammatory

CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and

CC antibodies that bind (I) are used in the manufacture of medicaments for

CC the treatment or prevention of infection or disease caused by

CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.

CC Nucleic acids encoding (I) are used to detect Streptococcus in a

CC biological sample. (I) is used to determine whether a compound binds to

CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be

CC used as a vaccine or diagnostic composition. The disease caused by

CC Streptococcus that is prevented or treated may be meningitis. Nucleic

CC acid encoding (I) may be used to recombinantly produce (I) and may be

CC used in gene therapy. Antibodies to (I) are used for affinity

CC chromatography, immunoassays, and distinguishing/identifying

CC Streptococcus proteins

XX Sequence 166 AA;

SQ

Query Match 44.2%; Score 151; DB 5; Length 166;  
Best Local Similarity 41.6%; Pred. No. 2.6e-10;  
Matches 32; Conservative 15; Mismatches 22; Indels 8; Gaps 2;

QY 1 EGEL-PAPLAGTV-----SKLVKGGDTVKAGOTVLVLKMKMETEINAPTGDGKVKV 52  
DB 89 EGDVIESPLVGVAFLAASDPKPFVAVGDTVKKQTLVLKMKVNEVPAPCDGVITEI 148

QY 53 LVKERDAVGGGGLIKI 69

DB 149 LVSNEDVIEFGGLVRI 165

Search completed: March 3, 2004, 10:29:13  
Job time : 37.4583 secs



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OM protein - protein search, using sw model

Run on: March 3, 2004, 10:26:14 ; Search time 17.7917 Seconds  
(without alignments)  
659.599 Million cell updates/sec

Title: US-09-987-485A-1  
Perfect score: 615  
Sequence: 1 MKLKVTNGTAYDQVDVVK.....KVLVKERDAVQGGGLIKIG 122

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78.\*  
1: Piri.\*  
2: Pir2.\*  
3: Pir3.\*  
4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	604.5	98.3	123	1 BKIP	biotin carboxyl ca
2	231.5	37.6	145	2 F75135	methylmalonyl-coa
3	221	35.9	149	2 A71074	probable methylmal
4	205	33.3	129	2 D49094	methylmalonyl-CoA
5	200.5	32.6	596	2 A28088	oxaloacetate decar
6	198.5	32.3	134	2 T44984	methylmalonyl-CoA
7	190.5	31.0	655	2 B70432	pyruvate carboxyla
8	190	30.9	140	2 H69526	methylmalonyl-CoA
9	187.5	30.5	599	2 D81367	probable pyruvate
10	185	30.1	597	2 G82308	oxaloacetate decar
11	184	29.9	571	2 F71133	probable oxaloacet
12	176.5	28.7	576	2 AC3038	biotin carboxylase
13	176.5	28.7	576	2 H98247	biotin carboxylase
14	176	28.6	134	2 C72341	propionyl-CoA carb
15	176	28.6	984	2 T44608	pyruvate carboxyla
16	175.5	28.5	591	2 B44465	sodium ion pump ox
17	175.5	28.5	610	2 G84306	biotin carboxylase
18	173.5	28.2	186	2 D90418	hypothetical prote
19	173.5	28.2	591	2 AB0509	oxaloacetate decar
20	173.5	28.2	591	2 AE0909	oxaloacetate decar
21	173	28.1	567	2 F64453	oxaloacetate decar
22	170	27.6	1144	2 D97227	pyruvate carboxyla
23	168.5	27.4	607	2 F82966	probable transcarb
24	168.5	27.4	620	2 F70439	oxaloacetate decar
25	166	27.0	600	2 F70980	probable accA3 pro
26	165	26.8	1150	2 A83378	pyruvate carboxyla
27	164	26.7	654	2 G87517	acetylpropionyl-C
28	163	26.5	142	2 D69510	oxaloacetate decar
29	163	26.5	598	2 G86999	hypothetical prote

30	163	26.5	598	2 A55579	biotin carboxyl ca
31	162	26.3	591	2 S71009	biotin carboxylase
32	162	26.3	597	2 S71006	biotin carboxylase
33	161.5	26.3	1174	2 AE2911	pyruvate carboxyla
34	161.5	26.3	1174	2 C97686	pyruvate carboxyla
35	159	25.9	665	2 G97819	hypothetical prote
36	158.5	25.8	593	2 B71373	probable oxaloacet
37	157	25.5	161	2 A95049	hypothetical prote
38	157	25.5	161	2 G97919	acetyl-CoA carboxy
39	157	25.5	170	2 F87482	hypothetical prote
40	157	25.5	1146	2 AC1565	pyruvate carboxyla
41	157	25.5	1146	2 AH1208	pyruvate carboxyla
42	156	25.4	1150	2 G89881	biotin carboxyl ca
43	155	25.2	167	2 T44291	methylcrotonoyl-Co
44	153.5	25.0	436	2 A53568	biotin carboxyl ca
45	152.5	24.8	162	2 A97521	biotin carboxyl ca

ALIGNMENTS

RESULT 1

PKIP  
biotin carboxyl carrier protein [validated] - Propionibacterium freudenreichii subsp. s.  
N:Alternate names: methylmalonyl-CoA carboxyltransferase biotin carboxyl carrier protei  
C:Species: Propionibacterium freudenreichii subsp. shermanii  
C:Date: 31-Mar-1980 #sequence\_revision 31-Mar-1980 #text\_change 01-Feb-2002  
C:Accession: A03401  
R:Maloy, W.L.; Bowien, B.U.; Zwolinski, G.K.; Kumar, K.G.; Wood, H.G.; Ericsson, L.H.;  
J. Biol. Chem. 254, 11615-11622, 1979  
A:Title: Amino acid sequence of the biotinyl subunit from transcarboxylase.  
A:Reference number: A03401; MUID:80049796; PMID:40985  
A:Accession: A03401  
A:Molecule type: protein  
A:Residues: 1-123 <MAL>  
C:Comment: Six or 12 chains of biotin carboxyl carrier protein (BCCP) are found in the  
onyl coenzyme A to BCCP and (2) from BCCP to pyruvate, forming oxalacetate.  
C:Comment: See PIR:A48665 and PIR:S36808.  
C:Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology  
C:Keywords: biotin binding  
F:50-123/Domain: lipoyl/biotin-binding homology <LPB>  
F:89/Binding site: biotin (lys) (covalent) #status experimental

Query Match	98.3%;	Score	604.5;	DB	1;	Length	123;
Best Local Similarity	99.2%;	Pred. No.	2.7e-41;				
Matches	122;	Conservative	0;	Mismatches	0;	Indels	1;
						Gaps	1;
QY	1	MKLKVTNGTAYD	V	D	V	D	V
		D	V	D	V	D	K
		K	S	H	E	N	P
		M	G	T	I	L	F
		F	G	G	T	G	G
		A	P	A	P	-	A
		A	G	C	A	G	A
		G	A	G	A	G	K
		A	G	E	G	E	I
		P	A	P			
							59
Db	1	MKLKVTNGTAYD	V	D	V	D	V
		D	V	D	V	D	K
		K	S	H	E	N	P
		M	G	T	I	L	F
		F	G	G	T	G	G
		A	P	A	P	-	A
		A	G	C	A	G	A
		G	A	G	A	G	K
		A	G	E	G	E	I
		P	A	P			
							60
QY	60	LACTVSKILVKEG	D	T	V	K	A
		G	D	T	V	K	A
		Q	T	V	L	V	L
		E	A	M	K	M	E
		T	E	I	N	A	P
		T	D	G	K	V	K
		L	V	K	E	R	D
		A	V	Q	G	G	L
		I					
							119
Db	61	LACTVSKILVKEG	D	T	V	K	A
		Q	T	V	L	V	L
		E	A	M	K	M	E
		T	E	I	N	A	P
		T	D	G	K	V	K
		L	V	K	E	R	D
		A	V	Q	G	G	L
		I					
							120
QY	120	KIG	122				
Db	121	KIG	123				

RESULT 2

F75135  
methylmalonyl-coa decarboxylase gamma chain PAB1771 - Pyrococcus abyssi (strain Orsay)  
C:Species: Pyrococcus abyssi  
C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000  
C:Accession: F75135  
R:anonymous, Genoscope  
submitted to the EMBL Data Library, July 1999  
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str  
A:Reference number: A75001  
A:Accession: F75135  
A:Status: preliminary  
A:Molecule type: DNA

A;Residues: 1-145 <KAW>  
A;Cross-references: GB:A0248285; GB:AL096836; NID:G5458067; PIDN:CAB49799.1; PID:G545831  
A;Experimental source: strain Orsay  
C;Genetics:  
A;Gene: PAB1771  
C;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology

Query Match 37.6%; Score 231.5; DB 2; Length 145;  
Best Local Similarity 41.4%; Pred. No. 1.2e-11;  
Matches 60; Conservative 18; Mismatches 44; Indels 23; Gaps 3;

Qy 1 MKLKVTVNGTAYDVVDV-----VDKSH-----NPMGTILFGGTGGGAPA 40  
Db 1 MKKVTVNGKEYEVEVEVMPGKFRVLEGTIYEVEANLGVQAPVQVQVATPTPTPT 60

Qy 41 PA---AGGAGAGKAGEGEIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPT 97  
Db 61 PTPVQAPTPVQASENVVTPMPGKVLKLVQEGQQVKGQGLLLEAMKMETEINAPT 120

Qy 98 DGKVEKVLKRDVAVQGGGLIKIG 122  
Db 121 DGWKRIILVKEGDAVDGTGTLIELG 145

RESULT 3  
A71074  
probable methylmalonyl-CoA decarboxylase gamma chain - Pyrococcus horikoshii  
C;Species: Pyrococcus horikoshii  
C;Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 20-Jun-2000  
A;Accession: A71074  
R;Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Hino, Y.; Yamamoto, S.; Sekin  
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi  
DNA Res. 5, 55-76, 1998  
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a  
A;Reference number: A71000; MUID:98344137; PMID:9679194  
A;Accession: A71074  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-149 <KAW>  
A;Cross-references: GB:AP000005; NID:G3236132; PIDN:BA30387.1; PID:G3257704  
A;Experimental source: strain OR3  
A;Note: This accession replaces an interim accession for a sequence replaced by GenBank  
C;Genetics:  
A;Gene: PH1284  
C;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology  
F;76-149/Domain: lipoyl/biotin-binding homology <LPB>

Query Match 35.9%; Score 221; DB 2; Length 149;  
Best Local Similarity 36.3%; Pred. No. 8.3e-11;  
Matches 53; Conservative 21; Mismatches 48; Indels 24; Gaps 1;

Qy 1 MKLKVTVNGTAYDVVDV-----VDKSHENPMGTILFGGTG 36  
Db 4 MKKVTVNGKEYEVEVEVMPGKFRVLEGTIYEVEVTSAGFTSPKQVQVPTPTPAPA 63

Qy 37 GAPAPAGAGAGKAGEGEIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAP 96  
Db 64 PTPPTAPAPSSKTVTVSENVVSPMPGKVLRLVVRGDRVRVQGLLLEAMKMETEINAP 123

Qy 97 TDGKVEKVLKRDVAVQGGGLIKIG 122  
Db 124 RDGWKRIILVKEGDAVDGTGTLIELG 149

RESULT 4  
D49094  
methylmalonyl-CoA decarboxylase (EC 4.1.1.41) gamma chain - Veillonella parvula  
C;Species: Veillonella parvula  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 20-Aug-1999  
C;Accession: D49094  
R;Huder, J.B.; Dimroth, P.  
J. Biol. Chem. 268, 24564-24571, 1993  
A;Title: Sequence of the sodium ion pump methylmalonyl-CoA decarboxylase from Veillonell

A;Reference number: A49094; MUID:94043308; PMID:8227015  
A;Accession: D49094  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-129 <HUD>  
A;Cross-references: GB:L22208; NID:G415592; PIDN:AAC36823.1; PID:G415596  
C;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology  
C;Keywords: carbon-carbon lyase; carboxy-lyase  
F;57-129/Domain: lipoyl/biotin-binding homology <LPB>

Query Match 33.3%; Score 205; DB 2; Length 129;  
Best Local Similarity 39.4%; Pred. No. 1.3e-09;  
Matches 50; Conservative 15; Mismatches 56; Indels 6; Gaps 2;

Qy 2 KLVTVNGTAYDVVDVVDK-----HENPMGTILFGGTGGGAPAPAGAGAG---KAGEGE 55  
Db 3 KFNVTNGTAYDVEVEVKAAPAAAPKAAAPAPAPAPAPAPAPAPAPAPAPAPAPAG 62

Qy 56 IPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPT DGKVEKVLKRDVAVQGG 115  
Db 63 VKAPMPGKILSVASVAGQAVKGETLLILEAMKQNEIAPADHADVSEVRVSANQTVSTG 122

Qy 116 QGLIKIG 122  
Db 123 DMVVLG 129

RESULT 5  
A28088  
oxaloacetate decarboxylase (EC 4.1.1.3) alpha chain - Klebsiella pneumoniae  
N;Alternate names: oxalate beta-decarboxylase, alpha chain  
C;Species: Klebsiella pneumoniae  
C;Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 11-Jan-2002  
C;Accession: A28088  
R;Schwarz, E.; Oesterhelt, D.; Reinke, H.; Beyreuther, K.; Dimroth, P.  
J. Biol. Chem. 263, 9640-9645, 1988  
A;Title: The sodium ion translocating oxaloacetate decarboxylase of Klebsiella pneumoniae  
A;Reference number: A28088; MUID:88257085; PMID:2454915  
A;Accession: A28088  
A;Molecule type: DNA  
A;Residues: 1-596 <SCH>  
A;Cross-references: EMBL:J03885; NID:G149288; PIDN:AA25120.1; PID:G149289  
C;Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/bi  
C;Keywords: biotin binding; carbon-carbon lyase; carboxy-lyase; sodium pump  
F;523-596/Domain: lipoyl/biotin-binding homology <LPB>  
F;562/Binding site: biotin (lys) (covalent) #status predicted

Query Match 32.6%; Score 200.5; DB 2; Length 596;  
Best Local Similarity 52.9%; Pred. No. 1.4e-08;  
Matches 45; Conservative 10; Mismatches 29; Indels 1; Gaps 1;

Qy 38 APAPAGAGAGKAGEG-EIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAP 96  
Db 511 APAPAPAPAPAPAGAGTPVTPAPLAGTIVKVLASEGQTVAAAGEVLLILEAMKMETEIRAA 570

Qy 97 TDGKVEKVLKRDVAVQGGGLIKI 121  
Db 571 QAGTVRGIAVKGADAVAVGDTLMTL 595

RESULT 6  
T44984  
methylmalonyl-CoA decarboxylase (EC 4.1.1.41) gamma chain [imported] - Propionigenium  
C;Species: Propionigenium modestum  
C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
C;Accession: T44984  
R;Bott, M.; Pfister, K.; Burda, P.; Kalbermatter, O.; Woehlke, G.; Dimroth, P.  
Eur. J. Biochem. 250, 590-599, 1997  
A;Title: Methylmalonyl-CoA decarboxylase from Propionigenium modestum: Cloning and seq  
A;Reference number: 422888; MUID:98088990; PMID:9428714  
A;Accession: T44984  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA

A;Residues: 1-134 <BOT>  
 A;Cross-references: EMBL:AJ002015; NID:G2706397; PIDN:CAA05139.1; PID:G2706400  
 A;Experimental source: DSM 2376  
 C;Comment: Methylmalonyl-CoA decarboxylase catalyses the only energy-conserving step during l-CoA is coupled to the vectorial transport of Na<sup>+</sup> across the cytoplasmic membrane, then C;Genetics:  
 A;Note: mmdc  
 C;Complex: heterotetramer [validated, MUID:98088990]  
 C;Function:  
 A;Description: EC 4.1.1.41 [validated, MUID:98088990]  
 A;Note: specific activity up to 25 U/mg protein; Km value for (S)-methylmalonyl-CoA of a C;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology  
 C;Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 32.3%; Score 198.5; DB 2; Length 134;  
 Best Local Similarity 38.5%; Pred. No. 4.5e-09;  
 Matches 52; Conservative 12; Mismatches 44; Indels 27; Gaps 3;

Qy 4 KVTVNGTAYDVDVDKSHENPMGTILFGGTGG-----APAPAAG 44  
 Db 5 KVTVNGTAYDVAVE-----EMGAASVASAPAAPAAPAAPAPAPAPKTT 57

Qy 45 GAGAGKAGEGIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKV 104  
 Db 58 AAGAG-AGANTVTPMPGTILNVGCHAGDKVSKGDTLVVLEAMKMEINEMAPHDGVVSEV 116

Qy 105 LVKERDAVQGGGLI 119  
 Db 117 RVQQASVNVAGDILV 131

RESULT 7  
 B70432  
 pyruvate carboxylase c-terminal domain - Aquifex aeolicus  
 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
 A;Reference number: A70300; MUID:98196666; PMID:9537320  
 C;Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 18-Aug-2000  
 C;Accession: B70432  
 R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.  
 Nature 392, 353-358, 1998  
 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
 A;Reference number: A70300; MUID:98196666; PMID:9537320  
 C;Accession: B70432  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-655 <AQF>  
 A;Cross-references: GB:AE000744; NID:G2983891; PIDN:AA007445.1; PID:G2983894; GB:AE00065  
 A;Experimental source: strain VF5  
 C;Genetics:  
 A;Gene: PYCA  
 C;Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/biotin F;572-646/Domain: lipoyl/biotin-binding homology <LPB>  
 F;612/Binding site: biotin (lys) (covalent) #status predicted

Query Match 31.0%; Score 190.5; DB 2; Length 655;  
 Best Local Similarity 36.8%; Pred. No. 9.6e-08;  
 Matches 49; Conservative 19; Mismatches 52; Indels 13; Gaps 3;

Qy 2 KLKVTVNGTAYDVD-----VDVDKSH-----NPMGTILFGGTGGGAPAPAAGAGAG 49  
 Db 513 KFKVRIEVSVDAESGPKPKYVYRNNRLEEIQLFKFAIPQGGGAQTVQSAEEEGIP 572

Qy 50 KAGE-GEIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLKE 108  
 Db 573 KATEPGDVTTPMPGKVVKILVKEGEPVQGGQTVATVTEAMKMEINEMAPHDGVVSEV 632

Qy 109 RDAVQGGGLI 121  
 Db 633 GDQVNPDAQIMRI 645

RESULT 8  
 H69526

methylmalonyl-CoA decarboxylase, biotin carboxyl carrier subunit (mmdc) homolog - Archia  
 C;Species: Archaeoglobus fulgidus  
 C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Aug-1999  
 C;Accession: H69526  
 R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodso  
 .; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F  
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
 Nature 390, 364-370, 1997  
 A;Authors: Overbeek, R.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S  
 Smith, H.O.; Woese, C.R.; Venter, J.C.  
 A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae  
 A;Reference number: A69250; MUID:98049343; PMID:9389475  
 A;Accession: H69526  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-140 <KLE>  
 A;Cross-references: GB:AE000952; GB:AE000782; NID:G2689275; PIDN:AA889036.1; PID:G264883  
 C;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology  
 F;67-140/Domain: lipoyl/biotin-binding homology <LPB>

Query Match 30.9%; Score 190; DB 2; Length 140;  
 Best Local Similarity 35.1%; Pred. No. 2.2e-08;  
 Matches 52; Conservative 19; Mismatches 37; Indels 40; Gaps 4;

Qy 1 MKLVTVNGTAYDVDVDKSHENPMGTILFGGTGGGAPA----- 40  
 Db 1 MKYEVKQKKYEVVE-----EVSFM---VFEVKVNGKAVIEVKKFEKFEKADIRE 53

Qy 41 -----PAAGGAGAGKAGEGIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMET 91  
 Db 54 RFAERREARAEVKAATGKA-----ITAPMAGVTVTKILKVKGEKVKAGETVLIIIEAMKME 109

Qy 92 EINAPTQKVEKVLVKERDAVQGGGLI 119  
 Db 110 PIASPEDETAIVVKEGDKVASGDVILV 137

RESULT 9  
 D81367  
 probable pyruvate carboxylase (EC 6.4.1.1) B chain Cj0933c [imported] - Campylobacter j  
 C;Species: Campylobacter jejuni  
 C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 03-Jun-2002  
 C;Accession: D81367  
 R;Parkhill, J.; Ween, B.W.; Mungall, K.; Kettle, J.M.; Churcher, C.; Basham, D.; Chilli  
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre  
 Nature 403, 665-668, 2000  
 A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals by  
 A;Reference number: A81250; MUID:20150912; PMID:10688204  
 A;Accession: D81367  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-599 <PAR>  
 A;Cross-references: GB:AL139076; GB:AL111168; NID:G6968128; PIDN:CAB73190.1; PID:G69683  
 A;Experimental source: serotype O2, strain NCTC 11168  
 C;Genetics:  
 A;Gene: PYCB; Cj0933c  
 C;Keywords: ligase

Query Match 30.5%; Score 187.5; DB 2; Length 599;  
 Best Local Similarity 37.5%; Pred. No. 1.5e-07;  
 Matches 48; Conservative 15; Mismatches 40; Indels 25; Gaps 3;

Qy 2 KLKVTVNGTAYDVDV-----VDVDKSHENPMGTILFGGTGGGAPAPAAGAGAGK 50  
 Db 481 KFTVAVNGKTHVEVSYGFDKDVNVKSVKVEENK-----NIISNSTSSVDA----- 528

Qy 51 AGEGEIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLKERD 110  
 Db 529 --ENEVLAGISGNVFKIYVNEGEEKSQAIWVLEAMKMEIENVAPKDGIIILELCIKGD 586

Qy 111 AVQGGQGL 118  
 Db 587 TVNEGEVL 594

**RESULT 12**

C:AC3038 biotin carboxylase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)	C:Species: Agrobacterium tumefaciens	C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AC3038	R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Wooldridge, G.; Gillet, W.; Grant, C.; Guentherer, D.; Kutayavin, T.; Levy, R.; Li, M.; McClelland, P.; Romero, P.; Zhang, S.	A:Karp, B.; Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, X.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.B.	A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.	A:Reference number: AB2577; PMID:21608550; PMID:11743193
A:Accession: AC3038	A>Status: preliminary	A:Molecule type: DNA
A:Residues: 1-576 <KUR>	A:Cross-references: GB:AEO08689; PIDN:AAU44721.1; PID:g17742353; GSPDB:GN00187	A:Experimental source: strain C58 (Dupont)
C:Genetics:	A:Gene: Atu3913	A:Map position: linear chromosome
C:Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lip	Query Match            28.7%; Score 176.5; DB 2; Length 576; Best Local Similarity 43.8%; Pred. No. 1.1e-06; Matches     42; Conservative     17; Mismatches     28; Indels         9; Gaps          3;	
QY      26 MGTLFGGGTGGAPAAPAGGAGAKAGEIPAPLAGTVSKILVKEGDVTVKAGQTVLVLE 85 :   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   : Db      488 LGIV--SGNASAPSAAV-----EKKEGEWTA PVSGTLQSFKVDGETVSEGDLLAVME 539		
QY      86 AMKMETEINAPTDCGVKKLVKVKERDAVQGCGGLIKI 121        ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   : Db      540 AMKMETQIVATRAKGK-VRLIVKEGYLQAQATLIDI 574		

**RESULT 13**

H98247 biotin carboxylase protein A2 [imported] - Agrobacterium tumefaciens (strain C58, Cerevisiae)	C:Species: Agrobacterium tumefaciens	C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C:Accession: H98247	R:Goodner, B.; Hinke, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldmarc, A.; Liu, F.; Wolian, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.	A:Science 294, 2233-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium t	A:Reference number: A97359; PMID:21608551; PMID:11743194	A:Status: preliminary
A:Cross-references: GB:AEO07870; PIDN:AAK89506.1; PID:g15159380; GSPDB:GN00170	A:Molecule type: DNA	A:Residues: 1-576 <KUR>
C:Genetics:	A:Gene: GR_L_1864	A:Map position: linear chromosome
C:Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lip	Query Match            28.7%; Score 176.5; DB 2; Length 576; Best Local Similarity 43.8%; Pred. No. 1.1e-06; Matches     42; Conservative     17; Mismatches     28; Indels         9; Gaps          3;	
QY      26 MGTLFGGGTGGAPAAPAGGAGAKAGEIPAPLAGTVSKILVKEGDVTVKAGQTVLVLE 85 :   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   : Db      488 LGIV--SGNASAPSAAV-----EKKEGEWTA PVSGTLQSFKVDGETVSEGDLLAVME 539		
QY      86 AMKMETEINAPTDCGVKKLVKVKERDAVQGCGGLIKI 121        ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   : Db      540 AMKMETQIVATRAKGK-VRLIVKEGYLQAQATLIDI 574		

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RESULT 14
C72341
propionyl-CoA carboxylase, gamma subunit - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: C72341
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: C72341
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-134 <ARN>
A:Cross-references: GB:AE001743; GB:AE000512; NID:g4981241; PIDN:AAD35799.1; PID:g498124
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0717
C:Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology

Query Match      28.6%; Score 176; DB 2; Length 134;
Best Local Similarity 33.6%; Pred. No. 2.8e-07;
Matches 49; Conservative 18; Mismatches 37; Indels 42; Gaps 4;

Qy 2 KLVTVNGTAYDVVDV-----VDKSH-----ENPMGTILFGGTGGA 38
Db 4 KFRVVNGKEVIEVEEIGNVRKPEAKPAKESQKTQVQIPKEEPVVL----- 55

Qy 39 PAPAAGGAGKAGGE---IPAPLAGTVSKTLVKEGTVKAGQTVLVLEAMKMETEINA 95
Db 56 -----EREKSSDQBEKLKAPWAGVILVVLVKEGQVNVGDKLLVFEAMKVENELQS 107

Qy 96 PTDGKVEKVLKRDVAVGGGGLIKI 121
Db 108 BFGTVKELVKEGDNIEGTQILNKI 133

RESULT 15
T44608
pyruvate carboxylase (EC 6.4.1.1) [imported] - Bacillus cereus (fragment)
C:Species: Bacillus cereus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 02-Sep-2000
C:Accession: T44608
R:Okstad, O.A.; Hegna, I.; Lindbaeck, T.; Rishovd, A.L.; Kolsto, A.B.
Microbiology 145, 621-631, 1999
A:Title: Genome organisation is not conserved between Bacillus cereus and Bacillus subtilis
A:Reference number: Z22811; MUID:99231848; PMID:10217496
A:Accession: T44608
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-984 <OKS>
A:Cross-references: EMBL:AJ010111; NID:g4584147; PIDN:CAB40604.1; PID:g4584148
A:Experimental source: ATCC 10987
C:Genetics:
A:Note: pyca
C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding
C:Keywords: ligase

Query Match      28.6%; Score 176; DB 2; Length 984;
Best Local Similarity 33.8%; Pred. No. 2e-06;
Matches 45; Conservative 19; Mismatches 49; Indels 20; Gaps 2;

Qy 9 GTAYDVVDVDKVS-----HENPMGTILFGGTGGAP-----APAGGAGA 48
Db 850 GEEIDVEIQKTLVYKLVISGSPQDGNRLVLEENGQPREIVVKDESVKATVAQRVKG 909

Qy 49 GKAGEGIEPAPLAGTVSKTLVKEGTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKE 108
Db 910 NRENPNHSAITMGTVKIVVVKEGDBVKKGSMAITAMKMETTVQAPFNGKVKYVND 969
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Qy 109 RDAVQGGGGLIKI 121
Db 970 GDAIQTGDLIEL 982

RESULT 16
B44465
sodium ion pump oxaloacetate decarboxylase subunit alpha - Salmonella typhimurium
C:Species: Salmonella typhimurium
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Aug-2000
C:Accession: B44465
R:Woehlike, G.; Wiffling, K.; Dimroth, P.
J. Biol. Chem. 267, 22798-22803, 1992
A:Title: Sequence of the sodium ion pump oxaloacetate decarboxylase from Salmonella typhimurium
A:Reference number: A44465; MUID:93054591; PMID:1331067
A:Accession: B44465
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-591 <WOE>
A:Cross-references: GB:M96434; NID:g154195; PIDN:AAA02973.1; PID:g408892
A:Experimental source: LT2
A:Note: sequence extracted from NCBI backbone
C:Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/biotin-binding site: biotin (lys) (covalent) #status: predicted
F:557/Binding site: biotin (lys) (covalent) #status: predicted

Query Match      28.5%; Score 175.5; DB 2; Length 591;
Best Local Similarity 37.5%; Pred. No. 1.3e-06;
Matches 48; Conservative 10; Mismatches 41; Indels 29; Gaps 3;

Qy 5 VTVNGTAYDVVDVDKSHENPMGTILFGG-----TGGAPAPAAGGAGKAGE 53
Db 481 VEVEGKAFVVKVS-----DGGDISQLTAAPPAASSAPVQAAAPAGAGT--- 523

Qy 54 GEIPAPLAGTVSKTLVKEGTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKEKRDVAVQ 113
Db 524 -PVTAPLAGNIWKVIATGEGTVAEQVLLILEAMKMETEIPAAQAGTVRGIAVKSQDAVS 582

Qy 114 GGGGLIKI 121
Db 583 VGDILMTL 590

RESULT 17
G84306
biotin carboxylase [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: G84306
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laaky, S.; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L
A:Title: Genome sequence of Halobacterium species NRC-1
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: G84306
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-610 <STO>
A:Cross-references: GB:AE004437; NID:g10581019; PIDN:AAG19819.1; GSPDB:GN00138
A:Gene: acc
C:Genetics:
C:Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoyl/biotin-binding site: biotin (lys) (covalent) #status: predicted
F:557/Binding site: biotin (lys) (covalent) #status: predicted

Query Match      28.5%; Score 175.5; DB 2; Length 610;
Best Local Similarity 38.1%; Pred. No. 1.4e-06;
Matches 48; Conservative 18; Mismatches 43; Indels 17; Gaps 5;

Qy 5 VTVNGTAYDVVDVDKSHENPMGTILFGG-----CTGGAPAPAAGGAGKAGE---GEGE- 55
Db 492 VEVNGKRFVNL-----ERGAQFAAPEADTGGGPPPEP-AGCADDGETWEGDGET 543
```



Best Local Similarity 50.7%; Pred. No. 2e-06;  
Matches 35; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 53 EGEIPAPLAGTISKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLKRDV 112  
DB 498 EGAVTSFPRGMVTKIKVKEGDKVKGDVIVVLEAMKMEHPESVPGTVERILIDGDAV 557

QY 113 QGQGGGLIKI 121  
DB 558 NVGDVIMII 566

RESULT 22  
D97227  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 30-Sep-2001  
C:Accession: D97227  
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: D97227  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1144 <XUR>  
A:Cross-references: GB:AE001437; PIDN:AAK80607.1; PID:g15025689; GSPDB:GN00168  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC2660  
C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding

Query Match 27.6%; Score 170; DB 2; Length 1144;  
Best Local Similarity 47.3%; Pred. No. 7.1e-06;  
Matches 35; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

QY 48 AGKAGEIEIPAPLAGTISKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLK 107  
DB 1070 ADSSNKEIGASIFGNVVKVFKPGDKVKKGDLSLMVTEAMKMETNVSVDGTVGGIFVK 1129

QY 108 ERDAVQGGGLIKI 121  
DB 1130 EGDQVQSGQLLVKL 1143

RESULT 23  
F82966  
C:Probable transcarboxylase subunit PA5435 [imported] - Pseudomonas aeruginosa (strain PAC)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: F82966  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Broman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: F82966  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-607 <STO>  
A:Cross-references: GB:AB004956; GB:AE004091; NID:g9951760; PIDN:AAG08820.1; GSPDB:GN00168  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA5435  
C:Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/biotin-binding

Query Match 27.4%; Score 168.5; DB 2; Length 607;  
Best Local Similarity 32.4%; Pred. No. 4.9e-06;  
Matches 44; Conservative 20; Mismatches 43; Indels 29; Gaps 3;

QY 5 VTVNGTAYDVVDV-----DVDKSHE-----NPMGTILFGGGTGAPAPAGG 45

DB 480 IDVHGTYRVDITGVGVKSDNKRHFYLSIDGMEPEVVFPLNEYVAGSASGRKHA----- 534

QY 46 AGAKAGAGEIEIPAPLAGTISKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVL 105  
DB 535 -----SEPHVSTTPGNTVDVLVKEGDSVKAGQAVLVTEAMKMETEIVQAGIAGTVKAIH 589

QY 106 VKERDAVQGGGLIKI 121  
DB 590 VAKGDRVNPGEILIEI 605

RESULT 24  
F70439  
C:Species: Aquifex aeolicus  
C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 18-Aug-2000  
C:Accession: F70439  
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'Neil, J.  
Nature 392, 353-358, 1998  
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A:Reference number: A70300; MUID:98196666; PMID:9537320  
A:Accession: F70439  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-620 <AQF>  
A:Cross-references: GB:AE000747; NID:g2983944; PIDN:AAC07497.1; PID:g2983949; GB:AE00061  
A:Experimental source: strain VF5  
C:Genetics:  
A:Gene: oadA  
C:Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/biotin-binding

Query Match 27.4%; Score 168.5; DB 2; Length 620;  
Best Local Similarity 33.8%; Pred. No. 5e-06;  
Matches 47; Conservative 17; Mismatches 52; Indels 23; Gaps 3;

QY 5 VTVNGTAYDVVDVVDKSHENPMGTILFGGGTGG-----APAPAGGA 46  
DB 475 VTVHGEQYHVQI-AGKGEEDPTRTFFIRLDGQLQVQLQPIREVSVKFAFAATEEGT 533

QY 47 GAGK-----AGEGEIPAPLAGTISKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVE 102  
DB 534 VISKRPKPKIGVTSPTGKVNKNVGVDEKVGEDVLLVLEAMKMEIHSPDQIVE 593

QY 103 KVLVKERDAVQGGGLIKI 121  
DB 594 EIFVRVGETVNPDEVLIRI 612

RESULT 25  
F70980  
C:Probable accA3 protein - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
C:Accession: F70980  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Sutherland, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
Nature 393, 537-544, 1998  
A:Authors: Squares, R.; Sutherland, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: F70980  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-600 <COL>  
A:Cross-references: GB:292771; GB:AL123456; NID:g3242259; PIDN:CAB07068.1; PID:g1877340  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: accA3

C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoyl F;527-600/Domain: lipoyl/biotin-binding homology <LFB>

Query Match 27.0%; Score 166; DB 2; Length 600;  
 Best Local Similarity 35.7%; Pred. No. 7.7e-06;  
 Matches 45; Conservative 18; Mismatches 51; Indels 12; Gaps 3;

QY 2 KLKVTNGTAYDVVDVVDKSHEN-----PMGTILFGGTTGGAPAPAAAGAGAGAGAGEGE- 55  
 Db 480 KVVVEIDGRVREVSLEADLALSNGGCDPVGV-----RRKPKPRKRGHTGAASGDA 533  
 QY 56 IPAPLAGTYSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLKRDVAVQGG 115  
 Db 534 VTPMQGTVVKFAVEGQEVVAGDLVVLEAMKMEPVTAHKDGTITGLAVEAGAILTQG 593  
 QY 116 QGLIKI 121  
 Db 594 TVLAEI 599

RESULT 26  
 A83978  
 C;Species: Bacillus halodurans  
 C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
 C;Accession: A83978  
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai  
 Nucleic Acids Res. 28, 4317-4331, 2000  
 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
 A;Reference number: A83650; MUID:20512582; PMID:11058132  
 A;Accession: A83978  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-1150 <STO>  
 A;Cross-references: GB:AP001516; GB:BA000004; NID:gl0175192; PIDN:BA06344.1; GSPDB:GN00  
 A;Experimental source: strain C-125  
 C;Genetics:  
 A;Gene: pyCA  
 C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding

Query Match 26.8%; Score 165; DB 2; Length 1150;  
 Best Local Similarity 47.3%; Pred. No. 1.8e-05;  
 Matches 35; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

QY 48 AGKAGEEIPAPLAGTYSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVK 107  
 Db 1074 ADKGNPNHIGASMGTVVKALVERKGVKQGDHLMITEAMKMEITVQAPDGEVVALHVK 1133  
 QY 108 ERDAVQGGGLIKI 121  
 Db 1134 DGDALQTGDLLEIV 1147

RESULT 27  
 G87517  
 C;Species: Caulobacter crescentus  
 C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
 C;Accession: G87517  
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
 B.; Laub, M.T.; DeBoij, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
 A;Title: Complete Genome Sequence of Caulobacter crescentus.  
 A;Reference number: A87249; MUID:21173698; PMID:11259647  
 A;Accession: G87517  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-654 <STO>  
 A;Cross-references: GB:AE005673; NID:gl3423663; PIDN:AAK24139.1; GSPDB:GN00148  
 C;Genetics:  
 A;Gene: CC2168  
 C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoyl

Query Match 26.7%; Score 164; DB 2; Length 654;  
 Best Local Similarity 31.0%; Pred. No. 1.2e-05;  
 Matches 48; Conservative 12; Mismatches 39; Indels 56; Gaps 4;

QY 1 MKLKVTNGTAYDVVDVVDKSHENPMGTILFGGTT-----TPLEVALIGGGTDSWDIRHADGSTFDEVTRLPPTY 35  
 Db 502 MHLPMSTDGKA----- 549  
 QY 36 GGAP-----APAAAGGAGAGAGAGEEIPAPLAGTYSKILVKEGDTVKAGQTV 81  
 Db 550 GKGP IQVFEGGVQBFDFVAKTGGAGGEGASGAILSPMPGKIVSVSVAGQTVSKGQIL 609  
 QY 82 LVLEAMKMETEINAPTDGKVEKVLKRDVAVQGG 116  
 Db 610 LTLEAMKMEHANAAPFDG-----VVAELSAVAGG 639

RESULT 28  
 D69510  
 C;Species: Archaeoglobus fulgidus  
 C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Aug-1999  
 C;Accession: D69510  
 R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodsc  
 .; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.E  
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
 Nature 390, 364-370, 1997  
 A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S  
 Smith, H.O.; Woese, C.R.; Venter, J.C.  
 A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae  
 A;Reference number: A69250; MUID:98049343; PMID:9389475  
 A;Accession: D69510  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-142 <LFB>  
 A;Cross-references: GB:AE000960; GB:AE000782; NID:92689283; PIDN:AB89171.1; PID:G26484  
 C;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology  
 F;66-139/Domain: lipoyl/biotin-binding homology <LFB>

Query Match 26.5%; Score 163; DB 2; Length 142;  
 Best Local Similarity 50.8%; Pred. No. 3.1e-06;  
 Matches 33; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 51 AGEGEIPAPLAGTYSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLKRD 110  
 Db 68 APENAVTSMPLPGVVLKILVKGKAGBPVVIVSMKMEINEIVSPTEGVVAAILVKEGQ 127  
 QY 111 AVOGG 115  
 Db 128 RIEAG 132

RESULT 29  
 G86999  
 C;Species: Mycobacterium leprae  
 C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
 C;Accession: G86999  
 R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; i  
 R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroy  
 eam, M.A.; Rutherford, K.M.  
 Nature 409, 1007-1011, 2001  
 A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S  
 Nature 409, 1007-1011, 2001  
 A;Title: Massive gene decay in the leprosy bacillus.  
 A;Reference number: A86909; MUID:21128732; PMID:11234002  
 A;Accession: G86999  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-598 <STO>  
 A;Cross-references: GB:AL450380; NID:gl3092853; PIDN:CAC30235.1; GSPDB:GN00147  
 C;Genetics:  
 A;Gene: bcca



C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoy

Query Match 26.5%; Score 163; DB 2; Length 598;  
Best Local Similarity 37.3%; Pred. No. 1.3e-05;  
Matches 44; Conservative 15; Mismatches 57; Indels 2; Gaps 2;

QY 5 VTVNGTAYDVVDVVDKSHENPMGTILFGGTTGGAPAPAAAGAGAGAGAGEGEIPAPLAGT 63  
DB 481 VEVDGRRLVSLPADLANAGNCP-AGVIRKKPKPRKRGHTGAATSGDAVTAPMQGT 539  
QY 64 VSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGGLIKI 121  
DB 540 VVKVAEGQTVMTGDLVVLEAMKMPVTAHKDGIITGLAVEAGTAITQGTVLAEI 597

## RESULT 30

A55579  
biotin carboxyl carrier protein - Mycobacterium leprae  
C;Species: Mycobacterium leprae  
C;Date: 25-Aug-1995 #sequence\_revision 25-Aug-1995 #text\_change 11-Jan-2002  
C;Accession: A55579; S22188  
R;Norman, E.; De Smet, K.A.L.; Stoker, N.G.; Ratledge, C.; Wheeler, P.R.; Dale, J.W.  
J. Bacteriol. 176, 2525-2531, 1994  
A;Title: Lipid synthesis in mycobacteria: characterization of the biotin carboxyl carrier  
A;Reference number: A55579; MUID:94222829; PMID:7909542  
A;Accession: A55579  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-598 <NOR>  
A;Cross-references: EMBL:X63470; NID:9443395; PIDN:CAA45070.1; PID:G581342  
C;Genetics:  
A;Start codon: GTG  
C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoy  
C;Keywords: biotin binding  
F;11-463/Domain: biotin carboxylase homology <BCH>  
F;525-598/Domain: lipoyl/biotin-binding homology <LPB>  
F;564/Binding site: biotin (lys) (covalent) #status predicted

Query Match 26.5%; Score 163; DB 2; Length 598;  
Best Local Similarity 37.3%; Pred. No. 1.3e-05;  
Matches 44; Conservative 15; Mismatches 57; Indels 2; Gaps 2;

QY 5 VTVNGTAYDVVDVVDKSHENPMGTILFGGTTGGAPAPAAAGAGAGAGAGEGE-IPAPLAGT 63  
DB 481 VEVDGRRLVSLPADLANAGNCP-AGVIRKKPKPRKRGHTGAATSGDAVTAPMQGT 539  
QY 64 VSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGGLIKI 121  
DB 540 VVKVAEGQTVMTGDLVVLEAMKMPVTAHKDGIITGLAVEAGTAITQGTVLAEI 597

## RESULT 31

A55579  
biotin carboxylase protein A2 - Saccharopolyspora erythraea  
C;Species: Saccharopolyspora erythraea  
C;Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 20-Jun-2000  
C;Accession: S71009  
R;Donadio, S.; Staver, M.J.; Katz, L.  
Mol. Microbiol. 19, 977-984, 1996  
A;Title: Erythromycin production in Saccharopolyspora erythraea does not require a function  
A;Reference number: S71005; MUID:96249691; PMID:8830278  
A;Accession: S71009  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-591 <DON>  
A;Cross-references: EMBL:X92557; NID:g1177651; PIDN:CAA63311.1; PID:g1177653  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995  
C;Genetics:  
A;Gene: bcpA2  
A;Start codon: GTG  
C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoy  
F;12-463/Domain: biotin carboxylase homology <BCH>  
F;517-590/Domain: lipoyl/biotin-binding homology <LPB>

Query Match 26.3%; Score 162; DB 2; Length 591;  
Best Local Similarity 35.9%; Pred. No. 1.6e-05;  
Matches 42; Conservative 18; Mismatches 51; Indels 6; Gaps 3;

QY 5 VTVNGTAYDVVDVVDKSHENPMGTILFGGTTGGAPAPAAAGAGAGAGAGEGEIPAPLAGTV 64  
DB 479 VEVGRRRLVSLPADLT---PAAAP--AGGAGRPRRSAGGGAGSSGDA-VTAPMQGTL 532  
QY 65 SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGGLIKI 121  
DB 533 VKLVVAEGSDRVSGDEIAVLEAMKMPVLAHKDGTVTGLTAQPGATLTQGSTLCEL 589

## RESULT 32

S71006  
biotin carboxylase protein A1 - Saccharopolyspora erythraea  
C;Species: Saccharopolyspora erythraea  
C;Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 20-Jun-2000  
C;Accession: S71006  
R;Donadio, S.; Staver, M.J.; Katz, L.  
Mol. Microbiol. 19, 977-984, 1996  
A;Title: Erythromycin production in Saccharopolyspora erythraea does not require a function  
A;Reference number: S71005; MUID:96249691; PMID:8830278  
A;Accession: S71006  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-597 <DON>  
A;Cross-references: EMBL:X92556; NID:g1177647; PIDN:CAA63308.1; PID:g1177649  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995  
C;Genetics:  
A;Gene: bcpA1  
A;Start codon: GTG  
C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoy  
F;18-469/Domain: biotin carboxylase homology <BCH>  
F;523-596/Domain: lipoyl/biotin-binding homology <LPB>

Query Match 26.3%; Score 162; DB 2; Length 597;  
Best Local Similarity 35.9%; Pred. No. 1.6e-05;  
Matches 42; Conservative 18; Mismatches 51; Indels 6; Gaps 3;

QY 5 VTVNGTAYDVVDVVDKSHENPMGTILFGGTTGGAPAPAAAGAGAGAGAGEGEIPAPLAGTV 64  
DB 485 VEVGRRRLVSLPADLT---PAAAP--AGGAGRPRRSAGGGAGSSGDA-VTAPMQGTL 538  
QY 65 SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGGLIKI 121  
DB 539 VKLVVAEGSDRVSGDEIAVLEAMKMPVLAHKDGTVTGLTAQPGATLTQGSTLCEL 595

## RESULT 33

AE2911  
pyruvate carboxylase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C;Species: Agrobacterium tumefaciens  
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
C;Accession: AE2911  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, J.; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan, Science 294, 2317-2323, 2001  
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A;Reference number: AE2577; MUID:21608550; PMID:11743193  
A;Accession: AE2911  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1174 <KUR>  
A;Cross-references: GB:AE008688; PIDN:AAL43707.1; PID:g17741236; GSPDB:GN00186  
A;Experimental source: strain C58 (Dupont)  
C;Genetics:  
A;Gene: pyca  
A;Map position: circular chromosome

C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding

Query Match 26.3%; Score 161.5; DB 2; Length 1174;  
Best Local Similarity 36.2%; Pred. No. 3.4e-05;  
Matches 47; Conservative 17; Mismatches 45; Indels 21; Gaps 5;

QY 2 KLVTVNGTAYDVVDVVDKSHENPMGTILFGGGTGGA-----PAAGGAGAGKAG 52  
DB 1050 KTLVIVNQASSGID---DKG---MVTVFF--EINGQPRRIKVPDRAHGASGSAVRRKAE 1100

QY 53 EG---EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQDKVEKVLVKER 109  
DB 1101 PGNASHIGAPMPGVISRVFINQOEKVGAGDVLVLSIEAMKMETALHAERDKIAEVLVKPG 1160

QY 110 DAVQGGQGLI 119  
DB 1161 DQIDAKDLII 1170

RESULT 34  
C97686  
pyruvate carboxylase (U51439) [imported] - Agrobacterium tumefaciens (strain C58, Cereon  
C:Species: Agrobacterium tumefaciens  
C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002  
C:Accession: C97686  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourullo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A:Reference number: A97359; MUID:21608551; PMID:11743194  
A:Accession: C97686  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1174 <KUR>  
A:Cross-references: GB:AE007869; PIDN:AAK88444.1; PID:g15157941; GSPDB:GN00169  
C:Genetics:  
A:Gene: AGR\_C\_4940  
A:Map position: circular chromosome  
C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding

Query Match 26.3%; Score 161.5; DB 2; Length 1174;  
Best Local Similarity 36.2%; Pred. No. 3.4e-05;  
Matches 47; Conservative 17; Mismatches 45; Indels 21; Gaps 5;

QY 2 KLVTVNGTAYDVVDVVDKSHENPMGTILFGGGTGGA-----PAAGGAGAGKAG 52  
DB 1050 KTLVIVNQASSGID---DKG---MVTVFF--EINGQPRRIKVPDRAHGASGSAVRRKAE 1100

QY 53 EG---EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQDKVEKVLVKER 109  
DB 1101 PGNASHIGAPMPGVISRVFINQOEKVGAGDVLVLSIEAMKMETALHAERDKIAEVLVKPG 1160

QY 110 DAVQGGQGLI 119  
DB 1161 DQIDAKDLII 1170

RESULT 35  
G97819  
hypothetical protein pccA [imported] - Rickettsia conorii (strain Malish 7)  
C:Species: Rickettsia conorii  
C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 22-Oct-2001  
C:Accession: G97819  
R:Ogata, H.; Audic, S.; Reneato-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R  
Science 293, 2093-2098, 2001  
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.  
A:Reference number: A97700; MUID:21442074; PMID:11557893  
A:Accession: G97819  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-665 <KUR>  
A:Cross-references: GB:AE006914; PIDN:AAL03497.1; PID:g15620071; GSPDB:GN00173  
C:Genetics:

A:Gene: pcca  
C:Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lip

Query Match 25.9%; Score 159; DB 2; Length 665;  
Best Local Similarity 50.0%; Pred. No. 3.1e-05;  
Matches 33; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 55 EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQDKVEKVLVKERDAVQG 114  
DB 598 EIQAFSLQIAIAIKVKEQEVTAQGEIMLLTAMKVENLLAERDCKIAKIFNEXDNVIR 657

QY 115 GQGLIK 120  
DB 658 GQVILE 663

RESULT 36  
B71373  
probable oxaloacetate decarboxylase, subunit alpha (oads) - syphilis spirochete  
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C:Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 18-Aug-2000  
C:Accession: B71373  
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gw  
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McI  
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998  
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
A:Reference number: A71250; MUID:98332770; PMID:9665976  
A:Accession: B71373  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-593 <COL>  
A:Cross-references: GB:AE001190; GB:AE000520; NID:g3322303; PIDN:AAC65051.1; PID:g3322  
A:Experimental source: strain Nichols  
C:Genetics:  
A:Gene: TP0056  
C:Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/bi

Query Match 25.8%; Score 158.5; DB 2; Length 593;  
Best Local Similarity 35.4%; Pred. No. 3e-05;  
Matches 45; Conservative 18; Mismatches 43; Indels 21; Gaps 3;

QY 6 TVNGTAYDVVDVVDKSHENPMGTILFGGGTGGA-----GAVLVNGTPTVTVVEAGPSVAGTSQGTVTAKVGACT 56  
DB 476 TVNGTAYTVVQE-----GAVLVNGTPTVTVVEAGPSVAGTSQGTVTAKVGACT 526

QY 57 --PAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQDKVEKVLVKERDAVQG 114  
DB 527 TLPAPVAGSVVXHTVQDGTATVNSGETVLMVESMKMELEVKATAAGTIH-FLIAPGAHVA 585

QY 115 GQGLIK 121  
DB 586 GQVLAEI 592

RESULT 37  
A95049  
hypothetical protein SP0423 [imported] - Streptococcus pneumoniae (strain TIGR4)  
C:Species: Streptococcus pneumoniae  
C:Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 24-Aug-2001  
C:Accession: A95049  
R:Tettein, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; He  
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzap  
son, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrisoi  
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A:Reference number: A95000; MUID:21357209; PMID:11463916  
A:Accession: A95049  
A:Status: preliminary  
A:Molecule type: DNA

```
C:Genetics:
A:Gene: Ccl183
C:Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology

Query Match      25.5%; Score 157; DB 2; Length 170;
Best Local Similarity 40.7%; Pred. No. 1.1e-05;
Matches 37; Conservative 16; Mismatches 30; Indels 8; Gaps 2;

QY    38  APAPAGGAGAGKAGGEIPAPLAGTV-----SKILVKEGDIVKAGOTVLVLKAMKE 90
       |||||:::||||:::||||:::||||:::||||:::||||:::||||:::||||
Db     80  APAFAVEAAPAVRGDA-VKSPWGTAYLSPQCADAFVKVGDTVAAGQTLLIVEANKTM 138
       |||||:::||||:::||||:::||||:::||||:::||||:::||||

QY    91  TEINAPTDCGVKVLKERDAVQGGGLIKI 121
       |||||:::||||:::||||:::||||:::||||:::||||:::||||
Db    139  NPAAAPKAGKIVVELVEDAQPVFEGPLVVI 169
       |||||:::||||:::||||:::||||:::||||:::||||:::||||

RESULT 40
AC1565
pyruvate carboxylase homolog pyCA [imported] - Listeria innocua (strain Clip112)
C:Species: Listeria innocua
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AC1565
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.;
   : Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.;
   D.: Jones, L.N.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournon, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.;
A>Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; PMID:21537279; PMID:11679669
A:Accession: AC1565
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1146 >GLA>
A:Cross-references: GB:AL592022; PIDN:CAC96291.1; PID:g16413519; GSPDB:GN00178
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: pyCA
C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin

Query Match      25.5%; Score 157; DB 2; Length 1146;
Best Local Similarity 43.9%; Pred. No. 7.6e-05;
Matches 29; Conservative 17; Mismatches 20; Indels 0; Gaps 0

QY    56  IPAPLAGTIVSKILVKEGDIVKAGOTVLVLKAMKETINAPTDCGVKVLKERDAVCGG 115
       :||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||
Db    1078  VGATMTGSVIQVVKKGSDSVKKGPDLITTEAMRKMETTIQAFPDEGVSSIVSGDGTIESG 113
       :||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||

QY    116  QGLIKI 121
       ||:::
Db    1138  DLLIEV 1143
       ||:::

Search completed: March 3, 2004, 10:31:48
Job time : 18.7917 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 3, 2004, 10:24:54 ; Search time 12.7083 Seconds  
(without alignments)  
499.873 Million cell updates/sec

Title: US-09-987-485A-1

Perfect score: 615

Sequence: 1 MKLKYTVNGTAYDVEDVDYDK.....KVLVYKRDVAVGGQGLIKIG 122

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	604.5	98.3	123	1 BCCP_PROFR	P02904 propionibac
2	200.5	32.6	595	1 DCOA_KLEPN	P13187 klebsiella
3	175.5	28.5	590	1 DCOA_SALTY	Q03030 salmonella
4	173	28.1	567	1 PYCB_WETJA	Q58628 methanococ
5	168	27.3	130	1 BCCP_STRMU	P29337 streptococ
6	163	26.5	598	1 BCCA_WCLE	P46392 mycobacteri
7	159	25.9	717	1 MCCA_MOUSE	Q99mr8 mus musculu
8	153	24.9	725	1 MCCA_HUMAN	Q96rq3 homo sapien
9	143	23.3	70	1 BCCP_LYCES	P05115 lycopersico
10	143	23.3	734	1 MCCA_ARATH	Q42523 arabidopsis
11	141	22.9	568	1 PYCB_WETTH	Q27179 methanobact
12	138.5	22.5	157	1 BCCP_PORPU	P51283 porphyra pu
13	138	22.4	1180	1 PYC2_YEAST	P23277 saccharomyc
14	133.5	21.7	163	1 BCCP_CHLMU	Q9pkrs chlamydia m
15	133	21.6	1178	1 BCCP_YEAST	P11154 saccharomyc
16	132	21.5	1189	1 PYC PIPCA	P78992 pichia past
17	131	21.3	164	1 BCCP_CHLTR	O84125 chlamydia t
18	130	21.1	629	1 ODP2_ECOLI	P06959 escherichia
19	130	21.1	731	1 MCCA_SOYBN	Q42783 glycine max
20	129.5	21.1	581	1 BCCP_ANASP	Q66881 anabaena sp
21	129	21.0	147	1 ODP2_PSEAE	Q59638 pseudomonas
22	129	21.0	1178	1 PYC_MOUSE	Q05920 mus musculu
23	128	20.8	544	1 ODP2_ACHLA	P35489 acholeplasm
24	125.5	20.4	654	1 BCCA_WCTTU	P46401 mycobacteri
25	123.5	20.1	637	1 ODP2_AZOVI	P10802 azotobacter
26	122	19.8	553	1 ODP2_ALCEU	Q59098 alcaligenes
27	121	19.7	1178	1 PYC_HUMAN	P11498 homo sapien
28	119	19.3	1178	1 PYC RAT	P52873 rattus norv
29	118.5	19.3	704	1 PCCE_RAT	P14882 rattus norv
30	118	19.2	70	1 BTB7_WYCSM	Q9xcd6 mycobacteri
31	117	19.0	156	1 BCCP_PSEAE	P37799 pseudomonas
32	115	18.7	70	1 BTB7_WYCTU	O05845 mycobacteri
33	115	18.7	262	1 BCCP_SOYBN	Q42783 glycine max

## RESULT 1

BCCP\_PROFR

ID\_BCCP\_PROFR STANDARD; PRT; 123 AA.

AC P02904;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Biotin carboxyl carrier protein of methylmalonyl-CoA carboxyl-

DE transferase (Transcarboxylase, 1.3S subunit).

OS Propionibacterium freudenreichii shermanii.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Propionibacteriaceae; Propionibacteriaceae; Propionibacterium.

OX NCBI\_TaxID=1752;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=85299212; PubMed=3898065;

RA Murtil V.L., Bahler C.R., Samols D.;

RT "Cloning and expression of the 1.3S biotin-containing subunit of

RT transcarboxylase.";

RL Proc. Natl. Acad. Sci. U.S.A. 82:5617-5621(1985).

RN [2]

RP SEQUENCE

RX MEDLINE=80049796; PubMed=40985;

RA Maloy W.L., Bowien B.U., Zwolinski G.K., Kumar G.K., Wood H.G.,

RA Ericsson L.H., Walsh K.A.;

RT "Amino acid sequence of the biotinyl subunit from transcarboxylase.";

RL J. Biol. Chem. 254:11615-11622(1979).

RN [3]

RP MUTAGENESIS OF ALA-87; MET-88; LYS-89 AND MET-90.

RX MEDLINE=92406744; PubMed=1526981;

RA Shenoy B.C., Xie Y., Park V.L., Kumar G.K., Beegen H., Wood H.G.,

RA Samols D.;

RT "The importance of methionine residues for the catalysis of the

RT biotin enzyme, transcarboxylase. Analysis by site-directed

RT mutagenesis.";

RL J. Biol. Chem. 267:18407-18412(1992).

RN [4]

RP STRUCTURE BY NMR.

RX MEDLINE=98066416; PubMed=9398186;

RA Reddy D.V., Shenoy B.C., Carey P.R., Soennichsen F.D.;

RT "Absence of observable biotin-protein interactions in the 1.3S

RT subunit of transcarboxylase: an NMR study.";

RL Biochemistry 36:14676-14682(1997).

CC BETWEEN THE SUBSTRATE BINDING SITES ON THE 12S AND 5S SUBUNITS.

CC -!- FUNCTION: THE BIOTINYL 1.3S SUBUNIT SERVES AS A CARBOXYL CARRIER

CC BETWEEN THE SUBSTRATE BINDING SITES ON THE 12S AND 5S SUBUNITS.

CC -!- SUBUNIT: TRANSCARBOXYLASE IS COMPOSED OF THREE SUBUNITS: 1.3S,

CC 5S, AND 12S. THE CORE OF THE ENZYME IS COMPOSED OF SIX 12S

CC SUBUNITS. ON EACH SIDE OF THE CORE THERE ARE THREE PAIRS OF 5S

CC SUBUNITS. EACH 5S DIMER IS ATTACHED TO THE CORE BY TWO 1.3S

CC SUBUNITS. THUS THE TOTAL NUMBER OF CHAINS IS 30 (6 + 12 + 12).

CC

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CC -----

CC EMBL; M11738; AAA25674.1; -

CC DR PIR; A03401; BKIP.

CC DR PDB; 1DC2; 10-MAY-00.

CC DR PDB; 1DD2; 24-MAR-00.

CC DR PDB; 1O78; 21-NOV-02.

CC DR InterPro; IPR001882; Biotin BS.

CC DR InterPro; IPR000089; Biotin\_lipoyl.

CC DR Pfam; PF00364; biotin\_lipoyl; 1.

CC DR PROSITE; PS00188; BIOTIN; 1.

CC KW Biotin; 3D-structure.

CC FT BINDING 89 89 BIOTIN.

CC SQ SEQUENCE 123 AA; 12367 MW; D0980C2065EA9A89 CRC64;

Query Match 98.3%; Score 604.5; DB 1; Length 123;

Best Local Similarity 99.2%; Pred. No. 6.1e-39;

Matches 122; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKLVTVNGTAYDVVDVVDKSHENPMGTILFGGTTGGAPAP-AAGGAGAGKAGEGETPAP 59

DB 1 MKLVTVNGTAYDVVDVVDKSHENPMGTILFGGTTGGAPAPRAAGGAGAGKAGEGETPAP 60

QY 60 LAGTVSKILVKEGTVKAGQTVLVLEAMKMETEINAPTGGKVKVVKERDAVGGGGLI 119

DB 61 LAGTVSKILVKEGTVKAGQTVLVLEAMKMETEINAPTGGKVKVVKERDAVGGGGLI 120

QY 120 KIG 122

DB 121 KIG 123

RESULT 2

DCOA KLEPN

ID DCOA KLEPN STANDARD; PRT; 595 AA.

AC P13187;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 01-JUL-1993 (Rel. 26, Last annotation update)

DE Oxaloacetate decarboxylase alpha chain (EC 4.1.1.3).

GN OADA.

OS Klebsiella pneumoniae.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Klebsiella.

OX NCBI\_TaxID=573;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88257085; PubMed=2454915;

RA Schwarz E., Cesterholt D., Reinke H., Beyreuther K., Dimroth P.;

RT "The sodium ion translocating oxalacetate decarboxylase of Klebsiella pneumoniae. Sequence of the biotin-containing alpha-subunit and relationship to other biotin-containing enzymes."

RL J. Biol. Chem. 263:9640-9645(1988).

CC -1- FUNCTION: Lyase and sodium transporter.

CC -1- CATALYTIC ACTIVITY: Oxaloacetate = pyruvate + CO(2).

CC -1- COFACTOR: Biotin and requires a sodium ion.

CC -1- SUBUNIT: Composed of three chains (alpha, beta, and gamma).

CC -----

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CC -----

CC EMBL; J03885; AAA25120.1; -

CC PIR; A28088; A28088.

CC HSP; P02905; IACX.

CC InterPro; IPR001882; Biotin BS.

CC InterPro; IPR000089; Biotin\_lipoyl.

CC InterPro; IPR000891; HMGL-like.

DR InterPro; IPR005776; Oada.

DR InterPro; IPR003379; PYC OADA.

DR Pfam; PF00364; biotin\_lipoyl; 1.

DR Pfam; PF00682; HMGL-like; 1.

DR Pfam; PF02436; PYC OADA; 1.

DR TIGRfams; TIGR01108; oada; 1.

DR PROSITE; PS00188; BIOTIN; 1.

KW Decarboxylase; Lyase; Sodium transport; Biotin.

FT INIT MET 0 0

FT BINDING 561 561 BIOTIN (BY SIMILARITY).

SQ SEQUENCE 595 AA; 63402 MW; AA744A95A6E9488C CRC64;

Query Match 32.6%; Score 200.5; DB 1; Length 595;

Best Local Similarity 52.9%; Pred. No. 4.4e-08;

Matches 45; Conservative 10; Mismatches 29; Indels 1; Gaps 1;

QY 38 APAPAGAGAGAGKAGEG-EIPAPLAGTVSKILVKEGTVKAGQTVLVLEAMKMETEINAP 96

DB 510 APAPAPAPAPAPAGAGTPTVPLAGTIWKVLASEGQTVAAAGEVLLILEAMKMETEIRAA 569

QY 97 TDGKVKVVKERDAVGGGGLI 121

DB 570 QAGTVRGIAVAGDAVAVGDTLMTL 594

RESULT 3

DCOA SALTY

ID DCOA SALTY STANDARD; PRT; 590 AA.

AC Q03030;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Oxaloacetate decarboxylase alpha chain (EC 4.1.1.3).

GN (OADA1 OR OADA2 OR STM0055) AND (OADA2 OR STM3352).

OS Salmonella typhimurium.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Salmonella.

OX NCBI\_TaxID=602;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=Lf2;

RX MEDLINE=93054591; PubMed=1331067;

RA Woehlike G., Wifling K., Dimroth P.;

RT "Sequence of the sodium ion pump oxaloacetate decarboxylase from Salmonella typhimurium."

RL J. Biol. Chem. 267:22798-22803(1992).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Lf2 / SGSC1412 / ATCC 700720;

RC MEDLINE=21534948; PubMed=11677609;

RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

RA "Complete genome sequence of Salmonella enterica serovar Typhimurium Lf2."

RL Nature 413:852-856(2001).

CC -1- FUNCTION: Lyase and sodium transporter.

CC -1- CATALYTIC ACTIVITY: Oxaloacetate = pyruvate + CO(2).

CC -1- COFACTOR: Biotin and requires a sodium ion.

CC -1- SUBUNIT: Composed of three chains (alpha, beta, and gamma).

CC -----

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CC -----

CC EMBL; M96434; AAA02973.1; -

CC EMBL; AE008696; AAL19019.1; -

```

DR EMBL; AE008854; AAL22221.1; -.
DR PIR; B44465; B44465.
DR HSP; P02905; 1A6X.
DR StyGene; SG10259; cadA1.
DR StyGene; SG7777; cadA2.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR005776; OadA.
DR InterPro; IPR003379; PYC OADA.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC OADA; 1.
DR TIGRFAMS; TIGR01108; oada; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR Decarboxylase; Lyase; Sodium transport; Biotin; Complete proteome.
FT INIT MET 0
FT BINDING 556 556 BIOTIN (BY SIMILARITY).
SQ SEQUENCE 590 AA; 63075 MW; 4EA421F9324AFD7B CRC64;

Query Match 28.5%; Score 175.5; DB 1; Length 590;
Best Local Similarity 37.5%; Pred. No. 3.2e-06;
Matches 48; Conservative 10; Mismatches 41; Indels 29; Gaps 3;

Qy 5 VTVNGTAYDVVDVSKSHENPMGTILFEGG-----TGCAPAPAGGAGKAGE 53
Db 480 VEVEGKAPVVKVS-----DGGDISQLTAAPVPAASAPVQAAPAGAGT--- 522

Qy 54 GEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQ 113
Db 523 -PVTAPLAGNIWKVIATIEGQTVASGDVLLILEAMKMETEIRAAAGTGVGIAVKSQDAVS 581

Qy 114 GQGGLIKI 121
Db 582 VGDITLMTL 589

RESULT 4
ID PYCB_METJUA STANDARD; PRT; 567 AA.
AC Q88628;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pyruvate carboxylase subunit B (EC 6.4.1.1) (Pyruvic carboxylase B).
GN PYCB OR MJ1231.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.D., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073 (1996).
[2]
RP SEQUENCE OF 190-125; 260-270; 277-289; 277-289; 309-325; 328-358;
RP 370-380; 386-409; 422-438; 491-506 AND 491-506, AND FUNCTION.
RX MEDLINE=21034791; PubMed=1195096;
RA Mukhopadhyay B., Patel V.J., Wolfe R.S.;
RT "A stable archaeal pyruvate carboxylase from the hyperthermophile
RT Methanococcus jannaschii."
RL Arch. Microbiol. 174:406-414 (2000).

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CC -1- FUNCTION: Pyruvate carboxylase catalyzes a 2-step reaction,
CC involving the ATP-dependent carboxylation of the covalently
CC attached biotin in the first step and the transfer of the carboxyl
CC group to pyruvate in the second.
CC -1- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3) (-) = ADP + phosphate +
CC oxaloacetate.
CC -1- COFACTOR: ATP, magnesium (or manganese or cobalt), pyruvate and
CC bicarbonate.
CC -1- ENZYME REGULATION: INHIBITED BY MAGNESIUM, WHEN ITS CONCENTRATION
CC EXCEEDED THE ATP ONE, AND BY HIGH CONCENTRATION OF ATP AND ALPHA-
CC KETOGLUTARATE.
CC -1- PATHWAY: Gluconeogenesis.
CC -1- SUBUNIT: Heterooctamer of four A and four B subunits.
CC -1- MASS SPECTROMETRY: MW=64160; METHOD=MALDI.
CC -1- MISCELLANEOUS: ITS OPTIMUM PH IS 8.5 AND THE OPTIMUM TEMPERATURE
CC IS 80-90 DEGREES CELSIUS.
CC -1- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
CC AND CARBAMYL PHOSPHATE SYNTHETASES.
CC -----
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CC -----
CC EMBL; U67563; AAB99233.1; -.
CC PIR; F64453; F64453.
CC HSP; P02905; 1A6X.
CC TIGR; MJ1231; -.
CC InterPro; IPR001882; Biotin_BS.
CC InterPro; IPR000089; Biotin_lipoyl.
CC InterPro; IPR000891; HMGL-like.
CC InterPro; IPR005776; OadA.
CC InterPro; IPR003379; PYC OADA.
CC Pfam; PF00364; biotin_lipoyl; 1.
CC Pfam; PF00682; HMGL-like; 1.
CC Pfam; PF02436; PYC OADA; 1.
CC TIGRFAMS; TIGR01108; oada; 1.
CC PROSITE; PS00188; BIOTIN; 1.
CC LIGase; Multifunctional enzyme; Gluconeogenesis; Magnesium; Pyruvate;
CC Biotin; Complete proteome.
CC BINDING 52 60 PYRUVATE (BY SIMILARITY).
CC BINDING 533 533 BIOTIN (BY SIMILARITY).
CC SEQUENCE 567 AA; 63907 MW; 5E07800622545628 CRC64;

Query Match 28.1%; Score 173; DB 1; Length 567;
Best Local Similarity 50.7%; Pred. No. 4.8e-06;
Matches 35; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

Qy 53 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 112
Db 498 EGAVTSPFRGMVTKIKVKEGDKVKGDVIVVLEAMKMEHPIESFVEGTVERILIDEGDAV 557

Qy 113 GQGGLIKI 121
Db 558 NVGDVIMI 566

RESULT 5
ID BCCP_STRMU STANDARD; PRT; 130 AA.
AC P29337;
DT 01-DEC-1992 (Rel. 24, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Biotin carboxyl carrier protein (BCCP).
GN BCC OR SMU1016.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;

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```

RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=UT-041 / Serotype C;
RX  MEDLINE=93159778; PubMed=8411283;
RA  Wang D., Waye M.M., Taricani M., Buckingham K., Sandham H.J.;
RT  "Biotin-containing protein as a cause of false positive clones in
RL  gene probing with streptavidin/biotin.";
RN  Biotechniques 14:209-212(1993).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=UA159 / ATCC 700610 / Serotype C;
RX  MEDLINE=22295063; PubMed=12397186;
RA  Ajdic D., McShan W.M., McLaughlin R.E., Savić G., Chang J.,
RT  Carson M.B., Primeaux C., Tian R., Keaton S., Jia H., Lin S., Qian Y.,
RA  Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferrretti J.J.;
RT  "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
RN  pathogen.";
RN  Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN=UT-041 / Serotype C;
RX  MEDLINE=22295063; PubMed=12397186;
RA  Ajdic D., McShan W.M., McLaughlin R.E., Savić G., Chang J.,
RT  Carson M.B., Primeaux C., Tian R., Keaton S., Jia H., Lin S., Qian Y.,
RA  Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferrretti J.J.;
RT  "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
RN  pathogen.";
RN  Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; M80523; AAA03702.1; -.
DR  EMBL; AE014941; AAN58716.1; -.
DR  HSSP; P02905; 1A6X.
DR  InterPro; IPR001882; Biotin_BS.
DR  InterPro; IPR000089; Biotin_lipoyl.
DR  Pfam; PF00364; biotin_lipoyl; 1.
DR  PROSITE; PS00188; BIOTIN; 1.
KW  Fatty acid biosynthesis; Biotin; Complete proteome.
FT  BINDING 96
FT  BINDING 96 N -> D (IN REF. 1).
FT  CONFLICT 121 121
SQ  SEQUENCE 130 AA; 13600 MW; ACDEA05EC46FF00B CRC64;
Query Match 27.38; Score 168; DB 1; Length 130;
Best Local Similarity 34.4%; Pred. No. 2.9e-06;
Matches 45; Conservative 18; Mismatches 52; Indels 16; Gaps 3;
QY 2 KLKVTNGVTAYDVDDVDKSHENPMGTIL--FGGGTGGG-----PAPAAGGAGAGK 50
DB 4 KFLSIDGKYLVEHEISSVPAATPIPTTENTFAASDQKQSQTPSPAATASAA-- 61
QY 51 AGSGEIPAPLAGTVSKILVKEGDTVKAGQTVLVEAMKMETEINAPTDGKVEKVLVKERD 110
DB 62 ---NTMPAPMGFTILKVLNVGDTVSENPQLMILEAMKMEIVAGMAGTVSAIHVSSGQ 118
QY 111 AVQGGQGLIKI 121
DB 119 TVNAGDNLIT 129
RESULT 6
ID _BCCA_MYCLE STANDARD; PRT; 598 AA.
AC P46392;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acetyl-/propionyl-coenzyme A carboxylase alpha chain [Includes: Biotin
DE carboxylase (EC 6.3.4.14); Biotin carboxyl carrier protein (BCCP)].
GN BCCA OR ML0726 OR B1308 Cl. 129.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
RN [1]
RX NCBI_TaxID=1769;
RP SEQUENCE FROM N.A.
RX MEDLINE=94222829; PubMed=7909542;

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```

RA Norman E., de Smet K.A.L., Stoker N.G., Ratledge C., Wheeler P.R.,
RA Dale J.W.;
RT "Lipid synthesis in mycobacteria: characterization of the biotin
RT carboxyl carrier protein genes from Mycobacterium leprae and M.
RL tuberculosis.";
RT J. Bacteriol. 176:2525-2531(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Smith D.R., Robison K.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eigmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies K.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seager K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Bartell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC -!- FUNCTION: THIS PROTEIN CARRIES TWO FUNCTIONS: BIOTIN CARBOXYL
CC -!- CARRIER PROTEIN AND BIOTIN CARBOXYLTRANSFERASE.
CC -!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)
CC = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.
CC -!- COFACTOR: Biotin.
CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.
CC -!- SUBUNIT: MULTIMER COMPRISED OF 2 DIFFERENT SUBUNITS, THE LARGER
CC ONE (63/64 kDa) HAS BIOTIN CARBOXYLASE AND BIOTIN CARRIER
CC FUNCTIONS, WHILE THE SMALLER SUBUNIT POSSESSES CARBOXYLTRANSFERASE
CC AND SUBSTRATE BINDING ACTIVITY.
CC -!- SIMILARITY: TO OTHER BIOTIN-DEPENDENT ENZYMES AND CARBAMOYL-
CC PHOSPHATE SYNTHETASES.
CC -----
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CC -----
DR  EMBL; X63470; CAA45070.1; -.
DR  EMBL; U00012; AAA5920.1; -.
DR  EMBL; AL583919; CAC30235.1; -.
DR  PIR; A55579; A55579.
DR  PIR; G86999; G86999.
DR  HSSP; P24182; 1BNC.
DR  Leproma; ML0726; -.
DR  InterPro; IPR001882; Biotin_BS.
DR  InterPro; IPR005482; Biotin_carb_C.
DR  InterPro; IPR000089; Biotin_lipoyl.
DR  InterPro; IPR005479; Cphase_L_D2.
DR  InterPro; IPR005481; Cphase_L_N.
DR  Pfam; PF02785; Biotin_carb_C; 1.
DR  Pfam; PF00364; biotin_lipoyl; 1.
DR  Pfam; PF00289; Cphase_L_chain; 1.
DR  Pfam; PF02786; Cphase_L_D2; 1.
DR  PROSITE; PS00188; BIOTIN; 1.
DR  PROSITE; PS00866; CPSASE_1; 1.
DR  PROSITE; PS00867; CPSASE_2; 1.
KW  Fatty acid biosynthesis; Ligase; Biotin; Multifunctional enzyme;
KW ATP-binding; Complete proteome.
RN  DOMAIN 11 441
RN  DOMAIN 532 598
RN  NP_BIND 169 174
RN  NP_BIND 169 174 ATP (BY SIMILARITY).
RN  ACT_SITE 299 299 BY SIMILARITY.
RN  BINDING 564 564 BIOTIN (BY SIMILARITY).
RN  CONFLICT 30 30 D -> H (IN REF. 1).

```

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Ronaldo M.F., Casavant T.L., Scheetz T.E.,



647 APMTGTIEKVVKAGDRVKGAGSLMVMIAMKWEHTIKAPKDGRIKKVFFSE 697

RESULT 8

CC MCCA HUMAN STANDARD; PRT; 725 AA.

AC Q96RQ3; Q9H959; Q9NS97;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase alpha subunit). MCC1 OR MCCA.

GN Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

[1]

RP SEQUENCE FROM N.A., AND VARIANTS MCGI ARG-325 AND SER-385.

RX PubMed=11170888;

RA Gallardo M.E., Desviat L.R., Rodriguez J.M., Esparza-Gordillo J., Perez-Cerdá C., Perez B., Rodriguez-Pombo P., Criado O., Sanz R., Morton D.H., Gibson K.M., Le T.P., Ribes A., Rodriguez de Cordoba S., Ugarte M., Penálva M.A.;

RA "The molecular basis of 3-methylcrotonylglycinuria, a disorder of leucine catabolism";

RT Am. J. Hum. Genet. 68:334-346 (2001).

RL [2]

RP SEQUENCE FROM N.A., AND VARIANT HIS-464.

RX MEDLINE=21295033; PubMed=11401427;

RA Oata K., Fukuda T., Morishita R., Abe S., Asakawa S., Yamaguchi S., Yoshino M., Ihara K., Murayama K., Shigemoto K., Shinizu N., Kondo I.;

RA "Human biotin-containing subunit of 3-methylcrotonyl-CoA carboxylase gene (MCCA): cDNA sequence, genomic organization, localization to chromosome band 3q27, and expression";

RT Genomics 72:145-152 (2001).

RL [3]

RP SEQUENCE FROM N.A., AND VARIANT MCGI PHE-535.

RX MEDLINE=21299419; PubMed=11406611;

RA Holzinger A., Roeschinger W., Lagler F., Mayerhofer P.U., Lichtner P., Kattenfeld T., Thuy L.P., Nyhan W.L., Koch H.G., Muntau A.C., Roscher A.A.;

RA "Cloning of the human MCCA and MCB genes and mutations therein reveal the molecular cause of 3-methylcrotonyl-CoA: carboxylase deficiency";

RT Hum. Mol. Genet. 10:1299-1306 (2001).

RL [4]

RP SEQUENCE FROM N.A., AND VARIANTS MCGI VAL-289; SER-385; PRO-437 AND HIS-532.

RX PubMed=11181649;

RA Baumgartner M.R., Almaashan S., Suormala T., Obie C., Cole R.N., Packman S., Baumgartner E.R., Valle D.;

RA "The molecular basis of human 3-methylcrotonyl-CoA carboxylase deficiency";

RT J. Clin. Invest. 107:495-504 (2001).

RL [5]

RP SEQUENCE FROM N.A.

RA Isogai T., Oka T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y., Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahashi K., Masuho Y., Sasaki N.;

RA "NEDO human cDNA sequencing project";

RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RL [6]

RP SEQUENCE FROM N.A.

RC TISSUE=Skeletal muscle;

RX MEDLINE=22389257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RL [7]

CC -1- CATALYTIC ACTIVITY: ATP + 3-methylcrotonyl-CoA + HCO(3)(-) = ADP + phosphate + 3-methylglutaconyl-CoA.

CC -1- COFACTOR: Biotin.

CC -1- PATHWAY: Leucine catabolism.

CC -1- SUBUNIT: Probably a dodecamer composed of six biotin-containing alpha subunits and six beta subunits.

CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.

CC -1- DISEASE: Defects in MCCC1 are the cause of 3-methylcrotonylglycinuria type I (MCGI) [MIM:210200]; also designated CGA or CG2. MCGI is a recessive disease that is characterized by muscular hypotonia and atrophy, probably of spinal origin.

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CC -----

DR EMBL; AF310972; AAG53095.1; -

DR EMBL; AB029826; BAA99407.1; -

DR EMBL; AF297332; AAK57986.1; -

DR EMBL; AF310339; AAG50245.1; -

DR EMBL; AK023051; BAB14377.1; -

DR EMBL; BC004214; AAH04214.1; -

DR EMBL; BC004187; AAH04187.1; -

DR GenBank; HGNC:6936; MCCC1.

DR GK; O96R03; -

DR MIM; 210200; -

DR GO; GO:0005759; C:mitochondrial matrix; NAS.

DR GO; GO:0009374; F:biotin binding; NAS.

DR GO; GO:0004485; F:methylcrotonyl-CoA carboxylase activity; NAS.

DR GO; GO:0006768; P:biotin metabolism; NAS.

DR GO; GO:0006552; P:leucine catabolism; NAS.

DR InterPro; IPR001882; Biotin\_BS.

DR InterPro; IPR005482; Biotin\_Carb\_C.

DR InterPro; IPR000089; Biotin\_lipoyl.

DR InterPro; IPR005479; Cphase\_L\_D2.

DR InterPro; IPR005481; Cphase\_L\_N.

DR Pfam; PF02785; Biotin\_carb\_C\_1.

DR Pfam; PF00364; biotin\_lipoyl\_1.

DR Pfam; PF00289; CPhase\_L\_chain\_1.

DR Pfam; PF02786; CPhase\_L\_D2\_1.

DR PROSITE; PS00188; BIOTIN; 1.

DR PROSITE; PS00867; CPhase\_2; 1.

DR Mitochondrion; Ligase; Biotin; ATP-binding; Transit peptide; Disease mutation; Polymorphism.

KW

FT TRANSIT 1 47 MITOCHONDRION (POTENTIAL).

FT CHAIN 48 725 METHYLCROTONYL-CoA CARBOXYLASE ALPHA CHAIN.

FT NP\_BIND 209 214 ATP (POTENTIAL).

FT ACT\_SITE 339 339 BY SIMILARITY.

FT BINDING 681 681 BIOTIN (BY SIMILARITY).

FT DOMAIN 538 541 POLY-SER.

FT DOMAIN 713 718 POLY-GLU.

FT VARIANT 289 289 A -> V (in MCGI; mild form).

FT VARIANT 325 325 /FTIQ=VAR 012785.  
 FT M -> R (in MCGI).  
 FT /FTIQ=VAR 012786.  
 FT VARIANT 385 385 R -> S (in MCGI; severe form).  
 FT /FTIQ=VAR 012787.  
 FT VARIANT 437 437 L -> P (in MCGI; severe form).  
 FT /FTIQ=VAR 012788.  
 FT VARIANT 464 464 P -> H.  
 FT /FTIQ=VAR 012789.  
 FT VARIANT 532 532 D -> H (in MCGI; severe form).  
 FT /FTIQ=VAR 012790.  
 FT VARIANT 535 535 S -> F (in MCGI; asymptomatic form).  
 FT /FTIQ=VAR 012791.  
 FT CONFLICT 469 469 F -> L (in REF. 3 AND 4).  
 FT SEQUENCE 725 AA; 80433 MW; B847C6B8060B6C0 CRC64;

Query Match 24.9%; Score 153; DB 1; Length 725;  
 Best Local Similarity 37.3%; Pred. No. 0.00019;  
 Matches 41; Conservative 17; Mismatches 42; Indels 10; Gaps 3;

QY 3 LKVTNGTAYDVDDVDSHPNMGITLFGGGTGG----APAPAAGGAGAGKAGGEIPA 58  
 DB 598 LKCSVNGVASKAKLII---LEN---TILFSEKGEIEIDIPVKYLSSVSSQETGGPLA 651  
 QY 59 PLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPDGGKVEKVLVKE 108  
 DB 652 PMGTGIEKVFVRAGDKVRAGDSLVMVMIAMKMBHTIKSPKDGTVKKVYFRE 701

RESULT 9  
 BCCP LYCES  
 ID BCCP LYCES STANDARD; PRT; 70 AA.  
 AC POS115;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 18-AUG-1987 (Rel. 05, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP)  
 DE (Fragment).  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC lamids; Solanales; Solanaceae; Solanum.  
 ON NCBI\_TaxID=4081;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87231088; PubMed=3588314;  
 RA Hoffman N.E., Pichersky E., Cashmore A.R.;  
 RA "A tomato cDNA encoding a biotin-binding protein."  
 RL Nucleic Acids Res. 15:3928-3928(1987).  
 CC -!- FUNCTION: This protein is a component of the acetyl coenzyme A  
 CC carboxylase complex; first, biotin carboxylase catalyzes the  
 CC carboxylation of the carrier protein and then the transcarboxylase  
 CC transfers the carboxyl group to form malonyl-CoA.  
 CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.  
 CC -!- SUBCELLULAR LOCATION: Chloroplast.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC DR EMBL; Y00144; CMA68339.1; -  
 CC DR HSP; P02905; LBPO.  
 CC DR InterPro; IPR001882; Biotin BS.  
 CC DR InterPro; IPR000089; Biotin lipoyl.  
 CC DR Pfam; PF00364; biotin lipoyl; 1.  
 CC DR PROSITE; PS00188; BIOTIN; 1.  
 KW Fatty acid biosynthesis; Biotin; Chloroplast.  
 FT NON\_TER 1 1  
 FT BINDING 35 35 BIOTIN (BY SIMILARITY).

SQ SEQUENCE 70 AA; 7416 MW; D75D018C0BD016BC CRC64;

Query Match 23.3%; Score 143; DB 1; Length 70;  
 Best Local Similarity 48.4%; Pred. No. 0.00012;  
 Matches 30; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 54 GEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPDGGKVEKVLVKE 113  
 DB 1 GTTVAPMVGLEVKVLKDGKVEQGPVLVLEAMKMEHVVKAPANGYVSGLEIKVGQSVO 60  
 QY 114 GG 115  
 DB 61 DG 62

RESULT 10  
 MCCA ARATH  
 ID MCCA ARATH STANDARD; PRT; 734 AA.  
 AC Q42523; Q9SA61;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor  
 DE (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha  
 DE subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase alpha subunit).  
 GN MCCA OR AT1G03090 OR F1003.8 OR F1003.9.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC euroids II; Brassicales; Brassicaceae; Arabidopsis.  
 ON NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC STRAIN=cv. Columbia;  
 EX MEDLINE=95232183; PubMed=7716229;  
 RA Weaver L.M., Lebrun L., Franklin A., Huang L., Hoffman N.,  
 RA Wurtele E.S., Nikolau B.J.;  
 RT "Molecular cloning of the biotinylated subunit of 3-methylcrotonyl-  
 RT coenzyme A carboxylase of Arabidopsis thaliana."  
 RL Plant Physiol. 107:1013-1014(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=21016719; PubMed=11130712;  
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
 RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,  
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Dewar K.,  
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
 RA Dunn P., Egtu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,  
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,  
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,  
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,  
 RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,  
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,  
 RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,  
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
 RT thaliana."  
 RL Nature 408:816-820(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=22954850; PubMed=14593172;  
 RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,  
 RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,  
 RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,  
 RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,  
 RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,  
 RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,







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RESULT 15
PVC1_YEAST
ID PYC1_YEAST STANDARD; PRT; 1178 AA.
AC P11154;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pyruvate carboxylase 1 (EC 6.4.1.1) (Pyruvic carboxylase 1) (PCB 1).
GN PYC1 OR PYV OR YGL062M.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE=88298405; PubMed=3042770;
RA Lim F., Morris C.P., Ochiodoro F., Wallace J.C.;
RT "Sequence and domain structure of yeast pyruvate carboxylase.";
RN J. Biol. Chem. 263:11493-11497(1988).
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=97377993; PubMed=9234674;
RA Feuermann M., de Montigny J., Potier S., Souciet J.-L.;
RT "The characterization of two new clusters of duplicated genes
RT suggests a 'Lego' organization of the yeast Saccharomyces cerevisiae
RT chromosomes."
RL Yeast 13:861-869(1997).
RN [3]
RP SEQUENCE OF 1003-1178 FROM N.A.
RX MEDLINE=87241529; PubMed=3036126;
RA Morris C.P., Lim F., Wallace J.C.;
RT "Yeast pyruvate carboxylase: gene isolation.";
RL Biochem. Biophys. Res. Commun. 145:390-396(1987).
CC -!- FUNCTION: Pyruvate carboxylase catalyzes a 2-step reaction,
CC involving the ATP-dependent carboxylation of the covalently
CC attached biotin in the first step and the transfer of the
CC carboxyl group to pyruvate in the second.
CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3) (-) = ADP + phosphate +
CC oxaloacetate.
CC -!- COFACTOR: Biotin and zinc.
CC -!- PATHWAY: Gluconeogenesis.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
CC AND CARBAMYL PHOSPHATE SYNTHETASES.
CC
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CC
CC EMBL; J03889; AAA34843.1; -.
CC EMBL; 272584; CAA96765.1; -.
CC PIR; S64066; QYBVP.
CC HSP; P24182; IENC.
CC GerMOnline; 141110; -.
CC SGD; S0003030; PYC1.
CC GO; GO:0005829; C:cytosol; IDA.
CC GO; GO:0004736; F:pyruvate carboxylase activity; IDA.
CC InterPro; IPR001862; Biotin_BS.
CC InterPro; IPR005482; Biotin_carb_C.
CC InterPro; IPR000089; Biotin_lipoyl.
CC InterPro; IPR005479; CPase_L_D.
CC InterPro; IPR005481; CPase_L_N.
CC InterPro; IPR000891; HMGL-like.
CC InterPro; IPR003379; PYC_OADA.
CC InterPro; IPR005930; Pyruv_carbox.
CC Pfam; PF02785; Biotin_carb_C; 1.
CC Pfam; PF00364; biotin_lipoyl; 1.

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DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRfam; TIGR01235; Pyruv carbox; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00866; CPSASE_1; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Ligase; Multifunctional enzyme; Biotin; Gluconeogenesis; ATP-binding;
KW Zinc; Multigene family.
FT NP BIND 182 187
FT ACT SITE 312 312
FT BINDING 1135 1135
FT CONFLICT 462 462
FT CONFLICT 493 493
FT CONFLICT 595 595
FT CONFLICT 619 619
FT CONFLICT 664 664
FT CONFLICT 772 772
FT CONFLICT 879 879
FT CONFLICT 903 909
FT CONFLICT 1178 AA; 130099 MW; BC7110A8AFB23E04 CRC64;
SQ
Query Match 21.6%; Score 133; DB 1; Length 1178;
Best Local Similarity 42.2%; Pred. No. 0.0092;
Matches 27; Conservative 15; Mismatches 22; Indels 0; Gaps 0;
QY 56 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKLVKRDVQGG 115
Db 1103 IGAPMAGVIVEVKVHGKSLIKKQGPVAVLSAMKMEMIISPSDGVKEVFSVDGNDVSS 1162
QY 116 QGLI 119
Db 1163 DLLV 1166

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RESULT 16
PVC_PICPA
ID PYC_PICPA STANDARD; PRT; 1189 AA.
AC P78992;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Pyruvate carboxylase (EC 6.4.1.1) (Pyruvic carboxylase) (PCB).
GN PYC1.
OS Pichia pastoris (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4922;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98301182; PubMed=9639311;
RA Menendez J., Delgado J., Gancedo C.;
RT "Isolation of the Pichia pastoris PYC1 gene encoding pyruvate
RT carboxylase and identification of a suppressor of the pyv
RT phenotype.";
RL Yeast 14:647-654(1998).
CC -!- FUNCTION: Pyruvate carboxylase catalyzes a 2-step reaction,
CC involving the ATP-dependent carboxylation of the covalently
CC attached biotin in the first step and the transfer of the
CC carboxyl group to pyruvate in the second (by similarity).
CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3) (-) = ADP + phosphate +
CC oxaloacetate.
CC -!- COFACTOR: Biotin and zinc.
CC -!- PATHWAY: Gluconeogenesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
CC AND CARBAMYL PHOSPHATE SYNTHETASES.
CC
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CC
CC EMBL; J03889; AAA34843.1; -.
CC EMBL; 272584; CAA96765.1; -.
CC PIR; S64066; QYBVP.
CC HSP; P24182; IENC.
CC GerMOnline; 141110; -.
CC SGD; S0003030; PYC1.
CC GO; GO:0005829; C:cytosol; IDA.
CC GO; GO:0004736; F:pyruvate carboxylase activity; IDA.
CC InterPro; IPR001862; Biotin_BS.
CC InterPro; IPR005482; Biotin_carb_C.
CC InterPro; IPR000089; Biotin_lipoyl.
CC InterPro; IPR005479; CPase_L_D.
CC InterPro; IPR005481; CPase_L_N.
CC InterPro; IPR000891; HMGL-like.
CC InterPro; IPR003379; PYC_OADA.
CC InterPro; IPR005930; Pyruv_carbox.
CC Pfam; PF02785; Biotin_carb_C; 1.
CC Pfam; PF00364; biotin_lipoyl; 1.

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DR EMBL; Y11106; CAA71993.1; -;  
 DR HSP; P24182; LDV1.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR InterPro; IPR005482; Biotin\_carb\_C.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR InterPro; IPR005483; CPhase\_L.  
 DR InterPro; IPR005479; CPhase\_L\_D2.  
 DR InterPro; IPR005481; CPhase\_L\_N.  
 DR InterPro; IPR000891; HMG-Like.  
 DR InterPro; IPR003379; PYC\_OADA.  
 DR InterPro; IPR005930; Pyruv\_carbox.  
 DR Pfam; PF02785; Biotin\_carb\_C; 1.  
 DR Pfam; PF00364; biotin\_lipoyl; 1.  
 DR Pfam; PF00289; CPhase\_L; 1.  
 DR Pfam; PF02786; CPhase\_L; 1.  
 DR Pfam; PF00682; HMG-Like; 1.  
 DR Pfam; PF02436; PYC\_OADA; 1.  
 DR Pfam; PF00098; CPhase.  
 DR TRFAMS; TIGR01235; Pyruv\_carbox; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 DR PROSITE; PS00866; CPhase\_1; 1.  
 DR PROSITE; PS00867; CPhase\_2; 1.  
 KW Ligase; Multifunctional enzyme; Biotin; Gluconeogenesis; ATP-binding;  
 KW Zinc.  
 FT NP\_BIND 185 190 ATP (POTENTIAL).  
 FT ACT\_SITE 315 315 BY SIMILARITY.  
 FT BINDING 1140 1140 BIOTIN (BY SIMILARITY).  
 SQ SEQUENCE 1189 AA; 131400 MW; 8B6E858079657914 CRC64;

Query Match 21.5%; Score 132; DB 1; Length 1189;  
 Best Local Similarity 46.6%; Pred. No. 0.011;  
 Matches 27; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

QY 55 EIPAPLAGTVSKILVKGDTVKAGQTVLVLEAMKMETEINAPTQDKVEKLVKRDV 112  
 DB 1107 EIGAPMAGVVEVHENGVEKGDPIAVLSAMKEMWISSPVAGRIGQIAVENDSV 1164

RESULT 17  
 BCCP\_CHLTR  
 ID\_BCCP\_CHLTR STANDARD; PRT; 164 AA.  
 AC 084125;2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP).  
 GN ACCEB OR CT123.  
 OS Chlamydia trachomatis.  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiales; Chlamydia.  
 OX NCBI\_TaxID=813;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=D/UM-3/Cx;  
 RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,  
 RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,  
 RA Davis R.W.;  
 RT "Genome sequence of an obligate intracellular pathogen of humans:  
 Chlamydia trachomatis.";  
 RL Science 282:754-759(1998).  
 CC -!- FUNCTION: This protein is a component of the acetyl coenzyme A  
 CC carboxylase complex; first, biotin carboxylase catalyzes the  
 CC carboxylation of the carrier protein and then the transcarboxylase  
 CC transfers the carboxyl group to form malonyl-CoA (By similarity).  
 CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.  
 CC -!- SUBUNIT: Homodimer (By similarity).

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DR EMBL; AB001286; AAC67714.1; -;  
 DR PIR; G71553; G71553.  
 DR HSP; P02905; 3BDO.  
 DR PHCI-2DPAGE; O84125; -;  
 DR InterPro; IPR001249; AcCoA\_biotinCC.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR Pfam; PF00364; biotin\_lipoyl; 1.  
 DR PRINTS; PR01071; AC0ABIORINCC.  
 DR TRFAMS; TIGR00531; BCCP; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 KW Fatty acid biosynthesis; Biotin; Complete proteome.  
 FT BINDING 128 128 BIOTIN (BY SIMILARITY).  
 SQ SEQUENCE 164 AA; 18198 MW; BD0BA4CEBC2D384C CRC64;

Query Match 21.3%; Score 131; DB 1; Length 164;  
 Best Local Similarity 28.2%; Pred. No. 0.0021;  
 Matches 40; Conservative 22; Mismatches 58; Indels 22; Gaps 4;

QY 2 KLVTVNGTAYDVEDVDKSHENPM--GTLFGGTTGGAPAPAAAGGAG-----AGKAGE 53  
 DB 20 RIVIKREGLELERDVTFSIQEPFYDNRFLFAGFSQERPIPTDQNLGNPIVKESIEKKE 79

QY 54 GEIPA-----PLAGTV-----SKLVKGGDTVKAGQTVLVLEAMKMETEINAPTQD 99  
 DB 80 SEAPAQGDFTVSLVGTFTYSGSPSEAPAFIKPGDVTSEDTVCIVEMKVMNEVKAGMSG 139

QY 100 KVEKLVKRDVAVQGGGLIKI 121  
 DB 140 RVEEILITGDPVQFGSKLFRI 161

# RESULT 18

ODP2\_ECOLI  
 ID\_ODP2\_ECOLI STANDARD; PRT; 629 AA.  
 AC P06959;  
 DT 01-APR-1988 (Rel. 07, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase  
 DE complex (EC 2.3.1.12) (E2).  
 GN ACEF OR B0115.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RA MEDLINE=8323434; PubMed=6345153;  
 RA Stephens P.E., Darlison M.G., Lewis H.M., Guest J.R.;  
 RT "The pyruvate dehydrogenase complex of Escherichia coli K12.  
 RT Nucleotide sequence encoding the dihydrolipoamide acetyltransferase  
 RT component.";  
 RL Eur. J. Biochem. 133:481-489 (1983).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MGI1655;  
 RA MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1233-1238 (1997).  
 [3]  
 RP SEQUENCE OF 1-12.









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DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin carb C.
DR InterPro; IPR000089; Biotin lipoyl.
DR InterPro; IPR005479; CPase I D2.
DR InterPro; IPR005481; CPase L N.
DR InterPro; IPR000891; HMG-L-like.
DR InterPro; IPR003379; PYC_OADA.
DR InterPro; IPR005930; Pyruv. carbox.
DR Pfam; PF02785; Biotin carb C; 1.
DR Pfam; PF00364; biotin lipoyl; 1.
DR Pfam; PF00289; CPase L chain; 1.
DR Pfam; PF02786; CPase L D2; 1.
DR Pfam; PF00682; HMG-L-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRFAMs; TIGR01235; pyruv. carbox; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR Ligase; Multifunctional enzyme; Biotin; Manganese; Gluconogenesis;
KW ATP-binding; Mitochondrion; Lipid synthesis; Transit peptide.
FT TRANSIT 1 20 MITOCHONDRION (POTENTIAL).
FT CHAIN 21 1178 PYRUVATE CARBOXYLASE.
FT DOMAIN 21 549 PRUVATE CARBOXYLASE (BY SIMILARITY).
FT DOMAIN 550 1000 CARBOXYLTRANSFERASE (BY SIMILARITY).
FT DOMAIN 1096 1178 BIOTIN CARBOXYL CARRIER PROTEIN
(BY SIMILARITY).
FT NP_BIND 198 203 ATP (BY SIMILARITY).
FT ACT_SITE 328 328 BY SIMILARITY.
FT BINDING 1144 1144 BIOTIN (BY SIMILARITY).
FT SEQUENCE 1178 AA; 129684 MW; 14CEA0F9DA8B8127 CRC64;

Query Match 21.0%; Score 129; DB 1; Length 1178;
Best Local Similarity 40.6%; Pred. No. 0.018;
Matches 28; Conservative 14; Mismatches 27; Indels 0; Gaps 0;

QY 53 EGEIPAPLAGTWSKILVKEGDTVKAGTQVLVLEAMKMETEINAPTQKVEKVLKRDVAV 112
Db 1109 KGQIGAPMGPKVIDIKVAAGDKVAKQPLCVLSAMKMETVWTSPMEGTIRKVRVTKDML 1168

QY 113 QGQGLIKI 121
Db 1169 EGGDLILEI 1177

RESULT 23
ODP2_ACHLA STANDARD; PRT; 544 AA.
AC P35489;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydrilipoamide acetyltransferase component of pyruvate dehydrogenase
complex (EC 2.3.1.12) (E2).
GN PDHC.
OS Acholeplasma laidlawii.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Acholeplasma.
OX NCBI_TaxID=2148;
RN [1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=92138635; PubMed=1735725;
RA Wallbrant P., Tegman V., Jonsson B.-H., Wieslander A.;
RT "Identification and analysis of the genes coding for the putative
pyruvate dehydrogenase enzyme complex in Acholeplasma laidlawii.";
RL J. Bacteriol. 174:1388-1396(1992).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
conversion of pyruvate to acetyl-CoA and CO(2). It contains
multiple copies of three enzymatic components: pyruvate
dehydrogenase (E1), dihydrilipoamide acetyltransferase (E2) and
lipoamide dehydrogenase (E3).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrilipoamide = CoA + S-
acetyldihydrilipoamide.
CC -!- COFACTOR: Contains 2 covalently bound lipoyl cofactors
(Potential).
CC -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral

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```

CC symmetry (By similarity).
CC -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M81753; AAA21909.1; -.
DR PIR; C42653; C42653.
DR HSSP; P07016; 1C4T.
DR InterPro; IPR001078; 2Oxoacid_dh.
DR InterPro; IPR000089; Biotin lipoyl.
DR InterPro; IPR004167; E3 binding.
DR InterPro; IPR003016; Lipoyl_BS.
DR Pfam; PF00198; 2-oxoacid dh; 1.
DR Pfam; PF00364; biotin lipoyl; 2.
DR Pfam; PF02817; e3_binding; 1.
DR ProDom; PD001115; 2Oxoacid_dh; 1.
DR PROSITE; PS00189; LIPOYL; 2.
KW Glycolysis; Transferase; Acyltransferase; Lipoyl.
FT BINDING 42 42 LIPOYL (BY SIMILARITY).
FT BINDING 154 154 LIPOYL (BY SIMILARITY).
FT ACT_SITE 516 516 POTENTIAL.
FT SEQUENCE 544 AA; 57261 MW; 81E92D869CFD5424 CRC64;

Query Match 20.8%; Score 128; DB 1; Length 544;
Best Local Similarity 29.0%; Pred. No. 0.011;
Matches 42; Conservative 23; Mismatches 26; Gaps 4;

QY 2 KUKVTVNGTAYDVVDVVKSHENPMGTILF-----GGGTGGA-----PAPAAGGA 46
Db 46 ELPSPVDGTI--VSLGAKEGEIHYGQIIVITDDGTGTAPAAPAPAPQAQVSAPTAPAAPQ 103

QY 47 GAGKAGEGEI-----PAPLAGTWSKILVKEGDTVKAGTQVLVLEAMKMETEINAPT 97
Db 104 VAAPAAAGDIYDFKADIGEGIHGEGITLQWNEFKVGDVKVEGTLVVEIDKYNELPSV 163

QY 98 DGKVEKVLKRDVAVGGQGLIKIG 122
Db 164 DGTILKLGKAGEGEIHYGVTVLIG 188

RESULT 24
BCCA_MYCTU STANDARD; PRT; 654 AA.
ID BCCA_MYCTU
AC P46401;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Acetyl-/propionyl-coenzyme A carboxylase alpha chain [includes: Biotin
carboxylase (EC 6.3.4.14); Biotin carboxyl carrier protein (BCCP)].
GN ACCAL OR BCCA OR RV2501C OR MT2576 OR MTCV07A7.07C OR MB2529C.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765;
RN [1]
SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=Isolate 50410;
RX MEDLINE=94222829; PubMed=7905542;
RA Norman E., de Smet K.A.L., Stoker N.G., Ratledge C., Wheeler P.R.,
RA Dale J.W.;
RT "Lipid synthesis in mycobacteria: characterization of the biotin
carboxyl carrier protein genes from Mycobacterium leprae and M.
tuberculosis.";
RL J. Bacteriol. 176:2525-2531 (1994).
RN [2]

```

SEQUENCE FROM N.A.  
 RC SPECIES=M.tuberculosis; STRAIN=H37Rv;  
 RA MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne K., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sulston J.E., Taylor K., Whitehead S., Barrall B.G.;  
 RA "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence.";  
 RL Nature 393:537-544(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;  
 RX MEDLINE=22206494; PubMed=12218036;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Olson R., White O., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Kouri H., Gill J., Mikula A.,  
 RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;  
 RA "Whole-genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains.";  
 RL J. Bacteriol. 184:5479-5490(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=M.bovis; STRAIN=AF2122/97;  
 RX MEDLINE=22709107; PubMed=12788972;  
 RA Garnier T., Eigmeier K., Camus J.-C., Medina N., Mansoor H.,  
 RA Pryor M., Duhoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,  
 RA Harris B., Aklin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,  
 RA Parkhill J., Barrall B.G., Cole S.T., Gordon S.V., Hewinson R.G.;  
 RA "The complete genome sequence of Mycobacterium bovis.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).  
 CC -!- FUNCTION: THIS PROTEIN CARRIES TWO FUNCTIONS: BIOTIN CARBOXYL  
 CC CARRIER PROTEIN AND BIOTIN CARBOXYLTRANSFERASE.  
 CC -!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)  
 CC = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.  
 CC -!- COFACTOR: Biotin.  
 CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.  
 CC -!- SUBUNIT: MULTIMER COMPRISED OF 2 DIFFERENT SUBUNITS, THE LARGER  
 CC ONE (63/64 kDa) HAS BIOTIN CARBOXYLASE AND BIOTIN CARRIER  
 CC FUNCTIONS, WHILE THE SMALLER SUBUNIT POSSESSES CARBOXYLTRANSFERASE  
 CC AND SUBSTRATE BINDING ACTIVITY.  
 CC -!- SIMILARITY: TO OTHER BIOTIN-DEPENDENT ENZYMES AND CARBAMOYL-  
 CC PHOSPHATE SYNTHETASES.  
 CC -----  
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 CC -----  
 DR EMBL; Z19549; CAA79609.1; -;  
 DR EMBL; Z95556; CAB08919.1; -;  
 DR EMBL; AB007094; AAK4680.1; -;  
 DR EMBL; BX248342; CAD97390.1; -;  
 DR PIR; B55579; B55579.  
 DR HSSP; P24182; 1BNC.  
 DR TIGR; MT2576; -;  
 DR TubercuList; Rv2501c; -;  
 DR InterPro; IPR001882; Biotin BS.  
 DR InterPro; IPR005482; Biotin carb C.  
 DR InterPro; IPR005089; Biotin lipoyl.  
 DR InterPro; IPR005479; CPase\_L\_D2.  
 DR InterPro; IPR005481; CPase\_L\_N.  
 DR Pfam; PF02785; Biotin carb C; 1.  
 DR Pfam; PF00364; biotin lipoyl; 1.  
 DR Pfam; PF00289; CPase\_L\_chain; 1.

DR Pfam; PF02786; CPase\_L\_D2; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 DR PROSITE; PS00866; CPASE\_1; 1.  
 DR PROSITE; PS00867; CPASE\_2; 1.  
 KW Fatty acid biosynthesis; Ligase; Biotin; Multifunctional enzyme;  
 KW ATP-binding; Complete proteome.  
 FT DOMAIN 1 437 BIOTIN CARBOXYLASE.  
 FT DOMAIN 588 654 BIOTIN CARBOXYL CARRIER PROTEIN.  
 FT NP\_BIND 162 167 ATP (BY SIMILARITY).  
 FT ACT\_SITE 294 294 BY SIMILARITY.  
 FT BINDING 620 620 BIOTIN (BY SIMILARITY).  
 SQ SEQUENCE 654 AA; 70592 MW; 70592 MW; FFA0A1A46432CABF CRC64;  
 Query Match 20.4%; Score 125.5; DB 1; Length 654;  
 Best Local Similarity 40.8%; Pred. No. 0.019;  
 Matches 29; Conservative 14; Mismatches 27; Indels 1; Gaps 1;  
 Qy 51 AGEIEIPAPLAGTGVSKLVKEGDTVKGQTVKAGQTVLVLEAMKMETEINAPTDGKVKVLVVERD 110  
 Db 583 ARPAEVVSPMPGSGVIAQVESGQISAGDVVVVVVVEAMKMEHSLAPVSGRVQ-VLVSVGD 641  
 Qy 111 AVQGGQGLIKI 121  
 Db 642 QVKVEQLARI 652  
 RESULT 25  
 ODP2\_AZOVI STANDARD; PRT; 637 AA.  
 ID ODP2\_AZOVI STANDARD; PRT; 637 AA.  
 AC P10802;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Dihydropyrimidine acetyltransferase component of pyruvate dehydrogenase  
 DE complex (EC 2.3.1.12) (E2).  
 OS Azotobacter vinelandii.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Azotobacter.  
 CC NCBI\_TaxID=354;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 478;  
 RX MEDLINE=88271330; PubMed=3292237;  
 RA Hanemaaijer R., Janssen A., de Kok A., Veeger C.;  
 RT "The dihydropyrimidine acetyltransferase component of the pyruvate  
 RT dehydrogenase complex from Azotobacter vinelandii. Molecular cloning  
 RT and sequence analysis.";  
 RL Eur. J. Biochem. 174:593-599(1988).  
 RN [2]  
 RN SEQUENCE OF 1-15 AND 380-415.  
 RX MEDLINE=88082750; PubMed=3691494;  
 RA Hanemaaijer R., de Kok A., Jolles J., Veeger C.;  
 RT "The domain structure of the dihydropyrimidine acetyltransferase component  
 RT of the pyruvate dehydrogenase complex from Azotobacter vinelandii.";  
 RL Eur. J. Biochem. 169:245-252(1987).  
 RN [3]  
 RN LIPOYL DOMAIN CONFORMATION.  
 RX MEDLINE=89052887; PubMed=3191993;  
 RA Hanemaaijer R., Vervoort J., Westphal A.H., de Kok A., Veeger C.;  
 RT "Mobile sequences in the pyruvate dehydrogenase complex, the E2  
 RT component, the catalytic domain and the 2-oxoglutarate dehydrogenase  
 RT complex of Azotobacter vinelandii, as detected by 600 MHz 1H-NMR  
 RT spectroscopy.";  
 RL FEBS Lett. 240:205-210(1988).  
 RN [4]  
 RN X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 381-637.  
 RX MEDLINE=92196586; PubMed=1549782;  
 RA Mattevi A., Obmolova G., Schulze E., Kalk K.H., Westphal A.H.,  
 RA de Kok A., Hol W.G.J.;  
 RT "Atomic structure of the cubic core of the pyruvate dehydrogenase  
 RT multienzyme complex.";  
 RL Science 255:1544-1550(1992).  
 RN [5]

RP STRUCTURE BY NMR OF 1-78.  
RX MEDLINE=94222112; PubMed=8068086;  
RA Berg A., de Kok A., Vervoot J.;  
RT "Sequential 1H and 15N nuclear magnetic resonance assignments and  
RT secondary structure of the N-terminal lipoyl domain of the  
RT dihydrolipoyl transacetylase component of the pyruvate dehydrogenase  
RT complex from *Azotobacter vinelandii*.";  
RL Eur. J. Biochem. 221:187-100(1994).  
RN [6]  
RP STRUCTURE BY NMR OF 1-78.  
RX MEDLINE=97234563; PubMed=9119000;  
RA Berg A., Vervoot J., de Kok A.;  
RT "Three-dimensional structure in solution of the N-terminal lipoyl  
RT domain of the pyruvate dehydrogenase complex from *Azotobacter*  
RT *vinelandii*.";  
RL Eur. J. Biochem. 244:352-360(1997).  
RN [6]  
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall  
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains  
CC multiple copies of three enzymatic components: pyruvate  
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and  
CC lipoamide dehydrogenase (E3).  
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-  
CC acetyldihydrolipoamide.  
CC -!- COFACTOR: Contains 3 covalently bound lipoyl cofactors (By  
CC similarity).  
CC -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral  
CC symmetry.  
CC -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.  
CC -!- SIMILARITY: Contains 3 lipoyl-binding domains.  
CC -----  
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CC -----  
DR EMBL; X12455; CAA30987.1; ALT\_INIT.  
DR PIR; S01017; XXAV.  
DR PDB; 1EAA; 31-OCT-93.  
DR PDB; 1EAB; 31-OCT-93.  
DR PDB; 1EAC; 31-OCT-93.  
DR PDB; 1EAD; 31-OCT-93.  
DR PDB; 1EAE; 31-OCT-93.  
DR PDB; 1EAF; 31-OCT-93.  
DR PDB; 1IYU; 12-MAR-97.  
DR PDB; 1IYV; 12-MAR-97.  
DR PDB; 1DPB; 20-APR-95.  
DR PDB; 1DPC; 20-APR-95.  
DR PDB; 1DPD; 20-APR-95.  
DR InterPro; IPR001078; 2-oxoacid\_dh.  
DR InterPro; IPR006256; Acef.  
DR InterPro; IPR000089; Biotin\_lipoyl.  
DR InterPro; IPR004167; E3\_binding.  
DR InterPro; IPR003016; Lipoyl\_BS.  
DR Pfam; PF00198; 2-oxoacid\_dh; 1.  
DR Pfam; PF00364; biotin\_lipoyl; 3.  
DR Pfam; PF02817; e3\_binding; 1.  
DR ProDom; PD001115; 2-oxoacid dh; 1.  
DR TIGRfam; TIGR01348; PDHac\_trf\_long; 1.  
DR PROSITE; PS00189; LIPOYL; 3.  
KW Glycolysis; transferase; Acyltransferase; Repeat; Lipoyl;  
KW 3D-structure.  
FT INIT MET 0  
FT DOMAIN 1 326 LIPOYL BINDING.  
FT DOMAIN 327 380 E1/E3 BINDING.  
FT DOMAIN 381 637 CATALYTIC.  
FT BINDING 39 39 LIPOYL (POTENTIAL).  
FT BINDING 156 156 LIPOYL (POTENTIAL).  
FT BINDING 261 261 LIPOYL (POTENTIAL).  
FT REPEAT 1 115  
FT REPEAT 116 220

FT REPEAT 221 326  
FT ACT SITE 610 610 POTENTIAL.  
FT STRAND 2 5  
FT STRAND 12 18  
FT TURN 22 23  
FT STRAND 25 25  
FT STRAND 31 36  
FT STRAND 41 45  
FT STRAND 51 55  
FT TURN 59 60  
FT STRAND 62 64  
FT TURN 65 66  
FT STRAND 68 73  
FT STRAND 403 406  
FT HELIX 416 431  
FT STRAND 434 442  
FT HELIX 444 452  
FT TURN 453 453  
FT HELIX 454 459  
FT TURN 460 461  
FT HELIX 466 480  
FT STRAND 482 484  
FT TURN 490 491  
FT STRAND 495 497  
FT STRAND 503 505  
FT TURN 507 509  
FT TURN 510 511  
FT STRAND 512 514  
FT STRAND 517 518  
FT HELIX 521 523  
FT HELIX 526 541  
FT TURN 542 543  
FT HELIX 547 550  
FT STRAND 555 559  
FT TURN 561 563  
FT TURN 574 575  
FT STRAND 578 582  
FT STRAND 586 591  
FT STRAND 596 609  
FT TURN 610 612  
FT HELIX 615 630  
FT HELIX 632 637  
SQ SEQUENCE 637 AA; 64913 MW; D063B4A5A385F84 CRC64;  
Query Match 20.1%; Score 123.5; DB 1; Length 637;  
Best Local Similarity 34.8%; Pred. No. 0.027;  
Matches 31; Conservative 15; Mismatches 38; Indels 5; Gaps 1;  
QY 38 APAPAAAGGAGAGKAGEGEIPAPLAGTVSK-----ILVKEGDTVKAGQTVLVLEAMKQETE 92  
Db 101 APSFGASATPAPAAASQEVVRVDPDGSAGKARVIEVLVKAGDQVQASQSLIVLESKASME 160  
QY 93 INAPTDGKVEKVLVKERDAVQGGQGLIKI 121  
Db 161 IPSPASGWVESVAIQLNAEVGTGDLITL 189  
RESULT 26  
ODP2\_ALCEU  
ID ODP2\_ALCEU STANDARD; PRT; 553 AA.  
AC Q59038;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase  
DE complex (EC 2.3.1.12) (E2).  
GN PDHB.  
OS Alcaligenes eutrophus (Ralstonia eutropha).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Burkholderiaceae; Ralstonia.  
OX NCBI\_TaxID=510;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN-H16 / DSM 428 / ATCC 17699;  
RX MEDLINE=94292470; PubMed=8021225;  
RA Hein S., Steinbuechel A.;  
RT "Biochemical and molecular characterization of the Alcaligenes  
RT eutrophus pyruvate dehydrogenase complex and identification of a new  
RT type of dihydrolipoamide dehydrogenase.";  
RL J. Bacteriol. 176:4394-4408(1994).  
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall  
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains  
CC multiple copies of three enzymatic components: pyruvate  
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and  
CC lipoamide dehydrogenase (E3).  
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-  
CC acetyldihydrolipoamide.  
CC -!- COFACTOR: Contains 2 covalently bound lipoyl cofactors (By  
CC similarity).  
CC -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral  
CC symmetry.  
CC -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.  
CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.  
CC  
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CC  
CC EMBL: U09865; AAA21599.1; -  
DR PIR: B55514; B55514.  
DR HSP: P10802; 1DPC.  
DR InterPro: IPR001078; 2Oxoacid\_dh.  
DR InterPro: IPR006256; Acef  
DR InterPro: IPR000089; Biotin\_lipoyl.  
DR InterPro: IPR003016; Lipoyl\_BS.  
DR Pfam: PF00198; 2-oxoacid\_dh; 1.  
DR Pfam: PF00364; biotin\_lipoyl; 2.  
DR Pfam: PF00115; 2Oxoacid\_dh; 1.  
DR TIGRFAMs: TIGR03348; PHAc\_trf\_long; 1.  
DR PROSITE: PS00189; LIPOYL; 2.  
KW Glycolysis; Transferrase; Acyltransferase; Repeat; Lipoyl.  
FT BINDING 44 44 LIPOYL (BY SIMILARITY).  
FT BINDING 162 162 LIPOYL (BY SIMILARITY).  
FT ACT\_SITE 526 526 POTENTIAL.  
FT SEQUENCE 553 AA; 57338 MW; BF5D370CC60C3F12 CRC64;  
Query Match 19.8%; Score 122; DB 1; Length 553;  
Best Local Similarity 38.9%; Pred. No. 0.03;  
Matches 35; Conservative 12; Mismatches 35; Indels 8; Gaps 2;  
QY 38 APAPAGAGAGKAGEG--EIPAPLAG-----TVSKILVKEGDTVTKAGQTVLVLEAMKM 89  
DB 104 APAPAAAPAAAPAGAGGGTIEVKVPDIDGYDAVPVIEVHVKAGDINAEADVVTLESKA 163  
QY 90 ETEINAPDTGKVEKVLVKERDAVQGGGLI 119  
DB 164 TMDVSPQGVVKEVKVKGVDNVAEGTLIL 193  
RESULT 27  
PVC\_HUMAN  
ID -PVC\_HUMAN STANDARD; PRT; 1178 AA.  
AC P11498; Q16705;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Pyruvate carboxylase, mitochondrial precursor (EC 6.4.1.1) (Pyruvic  
DE carboxylase) (PCB).  
GN PC.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney, and Liver;  
RX MEDLINE=95002202; PubMed=7918683;  
RA Wexler I.D., Liu Y., Ligasaris M.V., Mandel S.K., Freytag S.O.,  
RA Yang B.-S., Lu T.-C., Kwon M., Patel M.S., Keir D.S.;  
RT "Primary amino acid sequence and structure of human pyruvate  
RT carboxylase.";  
RL Biochim. Biophys. Acta 1227:46-52(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=94324922; PubMed=8048912;  
RA Mackay N., Rigat B., Douglas C., Chen H.S., Robinson B.H.;  
RT "cDNA cloning of human kidney pyruvate carboxylase.";  
RL Biochem. Biophys. Res. Commun. 202:1009-1014(1994).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney, and Liver;  
RA Walker M.E., Jitrapakdee S., Val D.L., Wallace J.C.;  
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Suetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Sutterich A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [5]  
RP SEQUENCE OF 1083-1178 FROM N.A.  
RX MEDLINE=87212051; PubMed=355348;  
RA Lambonwah A.-M., Qian F., Gravel R.A.;  
RT "Sequence homology around the biotin-binding site of human propionyl-  
RT CoA carboxylase and pyruvate carboxylase.";  
RL Arch. Biochem. Biophys. 254:631-636(1987).  
RN [6]  
RP SEQUENCE OF 1135-1178 FROM N.A.  
RX MEDLINE=85030380; PubMed=6548474;  
RA Freytag S.O., Collier K.J.;  
RT "Molecular cloning of a cDNA for human pyruvate carboxylase.  
RT Structural relationship to other biotin-containing carboxylases and  
RT regulation of mRNA content in differentiating preadipocytes.";  
RL J. Biol. Chem. 259:12831-12837(1984).  
RN [7]  
RP VARIANTS PC DEFICIENCY THR-610 AND ILE-743.  
RX MEDLINE=98254451; PubMed=9585612;  
RA Carbone M.A., Mackay N., Ling M., Cole D.E.C., Douglas C., Rigat B.,  
RA Feigenbaum A., Clarke J.T.R., Haworth J.C., Greenberg C.R.,  
RA Seagrave L., Robinson B.H.;  
RT "American pyruvate carboxylase deficiency is associated with two  
RT distinct missense mutations.";  
RL Am. J. Hum. Genet. 62:1312-1319(1998).  
RN [8]  
RP VARIANTS PC DEFICIENCY ALA-145 AND CYS-451.

MEDLINE=98244401; PubMed=9585002;  
Wexler I.D., Kerr D.S., Du Y., Kaung M.M., Stephenson W., Lusk M.M.,  
Wapner R.S., Higgins J.J.:  
RT "Molecular characterization of pyruvate carboxylase deficiency in two  
conspanguineous families";  
Pediatr. Res. 43:579-584(1998).  
CC -i- FUNCTION: Pyruvate carboxylase catalyzes a 2-step reaction,  
involving the ATP-dependent carboxylation of the covalently  
attached biotin in the first step and the transfer of the  
carboxyl group to pyruvate in the second. Catalyzes in a tissue  
specific manner, the initial reactions of glucone (liver, kidney)  
and lipid (adipose tissue, liver, brain) synthesis from pyruvate.  
CC -i- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3) (-) = ADP + phosphate +  
oxaloacetate.  
CC -i- COFACTOR: Biotin and manganese.  
CC -i- PATHWAY: Gluconeogenesis and lipogenesis.  
CC -i- SUBUNIT: Homotetramer.  
CC -i- SUBCELLULAR LOCATION: Mitochondrial matrix.  
CC -i- DISEASE: Defects in PC are the cause of pyruvate carboxylase  
deficiency (PC deficiency) [MIM:266150]. PC deficiency leads to  
lactic acidosis, mental retardation and death. It occurs in three  
forms: mild or type A, severe neonatal or type B, and a very mild  
lactacidemia.  
CC -i- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES  
AND CARBAMYL PHOSPHATE SYNTHETASES.  
-----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; U04641; AAA99537.1; -;  
DR EMBL; S72370; AAB31500.1; -;  
DR EMBL; U30891; AAA82937.1; -;  
DR EMBL; BC011617; AAH11617.1; -;  
DR EMBL; M26122; AAA36423.1; -;  
DR EMBL; K02282; AAA60033.1; -;  
DR PIR; G01933; JC2460.  
DR HSP; P24182; IENC.  
DR Genew; HGNC:8636; PC.  
DR MIM; 266150; -;  
DR GO; GO:0005524; F:ATP binding; TAS.  
DR GO; GO:0009374; F:biotin binding; TAS.  
DR GO; GO:0047336; F:pyruvate carboxylase activity; TAS.  
DR InterPro; IPR001882; Biotin BS.  
DR InterPro; IPR005482; Biotin carb C.  
DR InterPro; IPR000088; Biotin\_lipoyl.  
DR InterPro; IPR003479; CPhase\_L\_D2.  
DR InterPro; IPR005481; CPhase\_L\_N.  
DR InterPro; IPR000891; HMGL-like.  
DR InterPro; IPR003379; PYC\_OADA.  
DR InterPro; IPR005930; Pyruv carbox.  
DR Pfam; PF02785; Biotin carb C; 1.  
DR Pfam; PF00364; biotin\_lipoyl; 1.  
DR Pfam; PF00289; CPSase\_L\_chain; 1.  
DR Pfam; PF02786; CPSase\_L\_D2; 1.  
DR Pfam; PF00682; HMGL-like; 1.  
DR Pfam; PF02436; PYC\_OADA; 1.  
DR TIGRFAM; TIGR01235; pyruv carbox; 1.  
DR PROSITE; PS00188; BIOTIN; 1.  
KW Ligase; Multifunctional enzyme; Biotin; Manganese; Gluconeogenesis;  
KW ATP-binding; Mitochondrial; Lipid synthesis; Transit peptide;  
KW Disease mutation.  
FT TRANSIT 1 20 MITOCHONDRION (POTENTIAL).  
FT CHAIN 21 1178 PYRUVATE CARBOXYLASE.  
FT DOMAIN 21 549 BIOTIN CARBOXYLASE (BY SIMILARITY).  
FT DOMAIN 550 1000 CARBOXYLTRANSFERASE (BY SIMILARITY).  
FT DOMAIN 1096 1178 BIOTIN CARBOXYL CARRIER PROTEIN  
(BY SIMILARITY).  
FT FT

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=89308766; PubMed=2745462;  
 RX Browner M.F., Taroni F., Sztul E., Rosenberg L.E.;  
 RA "Sequence analysis, biogenesis, and mitochondrial import of the  
 RT alpha-subunit of rat liver propionyl-CoA carboxylase.";  
 RL J. Biol. Chem. 264:12680-12685(1989).  
 RN [2]  
 RN REVISIONS.  
 RP Browner M.F., Taroni F., Sztul E., Rosenberg L.E.;  
 RA Submitted (FEB-1989) to the EMBL/GenBank/DBJ databases.  
 RL -1- CATALYTIC ACTIVITY: ATP + propanoyl-CoA + HCO(3)(-) = ADP +  
 CC phosphate + (S)-methylmalonyl-CoA.  
 CC -1- COFACTOR: Biotin.  
 CC -1- PATHWAY: Key enzyme in the catabolic pathway of odd-chain fatty  
 CC acids, isoleucine, threonine, methionine, and valine.  
 CC -1- SUBUNIT: Probably a dodecamer composed of six biotin-containing  
 CC alpha subunits and six beta subunits.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 CC -1- DISEASE: Propionic acidemia due to recessively inherited  
 CC deficiency of PCCase activity often causes life-threatening  
 CC ketosis and acidosis.  
 CC  
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 CC  
 CC EMBL; M22631; AAA88512.1; ALT\_SEQ.  
 CC HSP; P24182; 1DV1.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR InterPro; IPR005482; Biotin\_Carb\_C.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR InterPro; IPR005479; CPase\_L\_D2.  
 DR InterPro; IPR005481; CPase\_L\_N.  
 DR Pfam; PF02785; Biotin\_carb\_C; 1.  
 DR Pfam; PF00364; biotin\_lipoyl; 1.  
 DR Pfam; PF00289; CPase\_L\_chain; 1.  
 DR Pfam; PF02786; CPase\_L\_D2; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 DR PROSITE; PS00866; CPASE1; 1.  
 DR PROSITE; PS00867; CPASE2; 1.  
 DR Mitochondrion; Ligase; Biotin; ATP-binding; Transit peptide.  
 KW NON\_TER 1 1  
 FT TRANSIT <1 21 MITOCHONDRION.  
 FT CHAIN 22 704 PROPIONYL-CoA CARBOXYLASE ALPHA CHAIN.  
 FT NP\_BIND 199 204 ATP (POTENTIAL).  
 FT ACT\_SITE 329 329 BY SIMILARITY.  
 FT BINDING 670 670 BIOTIN (BY SIMILARITY).  
 SQ SEQUENCE 704 AA; 77711 MW; 36CEEC52DF2D2A8A CRC64;  
 Query Match 19.3%; Score 118.5; DB 1; Length 704;  
 Best Local Similarity 27.8%; Pred. No. 0.069; 51; Indels 37; Gaps 4;  
 Matches 42; Conservative 21; Mismatches 21; ----- 45  
 QY 8 NGTAYDVVDVDSH-----ENPMGTILFG--GTGGAPAPAGG----- 45  
 Db 553 NGFTFNVVDGSKLNTWTNWLASPLLSVNVDTQRTVQCLSPDAGNMSIQFLGTYYKV 612  
 QY 46 -----AGAGKAGEIEP-----APLAGTVSKILVKEGTVKAGTVLVLEAKOME 90  
 Db 613 HILTKLAELNFKMLEKPKVTSSVLSRSPKPGVWVAVSVKPGDMVAEGEICVIEAKMQ 672  
 QY 91 TEINAFDTGKVEKVLKRDVAVGGGGLIKI 121  
 Db 673 NSWTAGKMGKVLVHCKAGDTVGEGLLVEL 703  
 OC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 CC -1- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES  
 CC AND CARBAMYL PHOSPHATE SYNTHETASES.  
 CC  
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 CC  
 CC EMBL; U32314; AAA96256.1; --  
 CC EMBL; U36585; AAC52668.1; --  
 CC PIR; S68252; JC4391.  
 DR HSP; P24182; 1BNC.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR InterPro; IPR005482; Biotin\_Carb\_C.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR InterPro; IPR005479; CPase\_L\_D2.  
 DR InterPro; IPR005481; CPase\_L\_N.  
 DR InterPro; IPR000891; HMGL-like.  
 DR InterPro; IPR003379; PYC OADA.  
 DR InterPro; IPR005930; Pyruv. carbox.  
 DR Pfam; PF02785; Biotin\_Carb\_C; 1.  
 DR Pfam; PF00364; biotin\_lipoyl; 1.  
 DR Pfam; PF00289; CPase\_L\_chain; 1.  
 DR Pfam; PF02786; CPase\_L\_D2; 1.  
 DR Pfam; PF00682; HMGL-like; 1.  
 DR Pfam; PF02436; PYC OADA; 1.  
 DR TIGRfams; TIGR01235; pyruv carbox; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 DR Ligase; Multifunctional enzyme; Biotin; Manganese; Gluconeogenesis;  
 KW ATP-binding; Mitochondrion; Lipid synthesis; Transit peptide.  
 KW ATP-binding; Mitochondrion; (POTENTIAL).  
 FT TRANSIT 1 20 MITOCHONDRION (POTENTIAL).  
 FT CHAIN 21 1178 PYRUVATE CARBOXYLASE.  
 FT DOMAIN 21 549 BIOTIN CARBOXYLASE (BY SIMILARITY).  
 FT DOMAIN 550 1000 CARBOXYLTRANSFERASE (BY SIMILARITY).  
 FT DOMAIN 1096 1178 BIOTIN CARBOXYL CARRIER PROTEIN  
 FT (BY SIMILARITY).  
 FT NP\_BIND 198 203 ATP (BY SIMILARITY).  
 FT ACT\_SITE 328 328 BY SIMILARITY.  
 FT BINDING 1144 1144 BIOTIN (BY SIMILARITY).  
 FT CONFLICT 222 222 P -> S (IN REF. 2).  
 FT CONFLICT 866 866 D -> I (IN REF. 2).  
 FT CONFLICT 977 977 G -> R (IN REF. 2).  
 SQ SEQUENCE 1178 AA; 129699 MW; 8E5FA19BC132A8DD CRC64;  
 Query Match 19.3%; Score 119; DB 1; Length 1178;  
 Best Local Similarity 37.7%; Pred. No. 0.1; Mismatches 28; Indels 0; Gaps 0;  
 Matches 26; Conservative 15; ----- 117  
 QY 53 EGEIPAPLAGTVSKILVKEGTVKAGTVLVLEAKMTEINAPTDGKVEKVLKRDVAV 112  
 Db 1109 KGQIGAPMGKVIDVKVAGAKVVGQPLCVLSAMKNEIVVTSPEGTIRKVVHTKDWTL 1168  
 QY 113 QGGQGLIKI 121  
 Db 1169 EGDLLILEI 1177  
 RESULT 29  
 PCCA RAT STANDARD; PRT; 704 AA.  
 ID PCCA RAT  
 AC P14882;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Propionyl-CoA carboxylase alpha chain, mitochondrial precursor  
 DE (EC 6.4.1.3) (pCase alpha subunit) (Propanoyl-CoA:carbon dioxide  
 DE ligase alpha subunit) (Fragment).  
 GN PCCA.  
 OS Rattus norvegicus (Rat).



[illegible]

Best Local Similarity 37.7%; Pred. No. 0.015; Matches 23; Conservative 13; Mismatches 25; Indels 0; Gaps 0;

QY 55 ETPAPLAGTUSKLVKGGTQVLEAMKMETETINAPTDGKVEKVLKRDVQV 114  
Db 3 DVRAEIVASLVYVNEGDOIDKGVVLLSWMKEIPVLAEEAGTVSKVAVSGVDVQA 62  
QY 115 G 115  
Db 63 G 63

RESULT 33  
BCCP SOYBN STANDARD; PRT; 262 AA.  
ID BCCP SOYBN  
AC Q42783; 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Biotin carboxyl carrier protein of acetyl-CoA carboxylase, chloroplast  
DE precursor (BCCP).  
OS ACCB-1.  
GN Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OC NCBI\_TaxID=3847;  
OX [1]  
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RP STRAIN=cv. Resnik;  
RC Reverdatto S.V., Beilinson V., Neilson N.C.;  
RA "Characterization of a cDNA clone encoding a BCCP subunit of acetyl-  
RT (Co) plant Gene Register PCR96-040.  
RL In) Biotin carboxylase from soybean."  
CC [1] FUNCTION: This protein is a component of the acetyl coenzyme A  
CC carboxylase complex; first, biotin carboxylase catalyzes the  
CC carboxylation of the carrier protein and then the transcarboxylase  
CC transfers the carboxyl group to form malonyl-CoA.  
CC [1] PATHWAY: Long-chain fatty acid biosynthesis; first step.  
CC [1] SUBCELLULAR LOCATION: Chloroplast.  
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CC EMBL; U40666; AAB67836.1; -  
CC PIR; T06600; T06600.  
CC HSSP; P02905; 3BDO.  
CC InterPro; IPR001249; AcCoA\_biotinCC.  
CC InterPro; IPR001882; Biotin\_BS.  
CC InterPro; IPR000089; Biotin\_lipoyl.  
CC Pfam; PF00364; biotin\_lipoyl; 1.  
CC PRINTS; PR01071; AC0AB10TNC.  
CC TIGRFAMs; TIGR00531; BCCP; 1.  
CC PROSITE; PS00188; BIOTIN; 1.  
CC Fatty acid biosynthesis; Biotin; Chloroplast; Transit peptide.  
KW TRANSIT 1 47 CHLOROPLAST  
FT CHAIN 48 262 BIOTIN CARBOXYL CARRIER PROTEIN OF  
FT BINDING 227 227 BIOTIN-COA CARBOXYLASE.  
FT SEQUENCE 262 AA; 27657 MW; 79B273BD8B7DF48 CRC64;  
Query Match 18.7%; Score 115; DB 1; Length 262;  
Best Local Similarity 25.0%; Pred. No. 0.051;  
Matches 36; Conservative 24; Mismatches 46; Indels 38; Gaps 5;  
QY 1 MKLVTVGTAVDVVDVVKSH-----ENPMGTILFGGGTGGAP----- 39  
Db 114 LKLU-----QHDVEVTIRKEMPPFPAPQPSVVSPPPPALPPPPVPPASTPTLAR 167

QY	40	-APAGGAGAGAGEIP---	APLAGTVSK-----	ILVKEGDTVFKAGQTVLVLEAMK	98
Db	168	ATPTTSAPAVKSAKSLPLKSPMAGTFRSPAPGEPFVKVGDVKKGVVCIIEAMK	227		
QY	89	METEINAPTIDGKVKLVKRDV	112		
Db	228	LNNEIEADQSGTIVEIADKSV	251		
RESULT 34					
ODP2_MYCCA		STANDARD;	PRT;	438 AA.	
ID	ODP2_MYCCA				
AC	Q49110;				
DT	30-MAY-2000 (Rel. 39, Created)				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DT	30-MAY-2000 (Rel. 39, Last annotation update)				
DE	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) (E2).				
DE	complex (EC 2.3.1.12) (E2).				
GN	PDHC OR ODP2.				
OS	Mycoplasma capricolum.				
OC	Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.				
OX	NCBI_TaxID=2095;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	MEDLINE=97001869; PubMed=8844861;				
RX	Zhu P.P., Peterkofsky A.;				
RA	"Sequence and organization of genes encoding enzymes involved in pyruvate metabolism in Mycoplasma capricolum.";				
RT					
RL	Protein Sci. 5:1719-1736(1996).				
CC	-!- FUNCTION: THE PYRUVATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL CONVERSION OF PYRUVATE TO ACETYL-COA (CO2). IT CONTAINS MULTIPLE COPIES OF THREE ENZYMATIC COMPONENTS: PYRUVATE DEHYDROGENASE (E1), DIHYDROLIPOAMIDE ACETYLTRANSFERASE (E2) & LIPOAMIDE DEHYDROGENASE (E3) (BY SIMILARITY).				
CC	-!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-acetyldihydrolipoamide.				
CC	-!- COFACTOR: Contains 1 covalently bound lipoyl cofactor (By similarity).				
CC	-!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral symmetry (By similarity).				
CC	-!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.				
CC	-!- SIMILARITY: Contains 1 lipoyl-binding domain.				
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DR	EMBL; U62057; AAC4344.1; ..				
DR	HSP; P07016; 1C47.				
DR	InterPro; IPR001078; 2Oxoacid dh.				
DR	InterPro; IPR000089; Biotin lipoyl.				
DR	InterPro; IPR004167; E3 binding.				
DR	InterPro; IPR003016; Lipoyl BS.				
DR	Pfam; PF00198; 2-oxoacid dh; 1.				
DR	Pfam; PF00364; Biotin lipoyl; 1.				
DR	Pfam; PF02817; e3 binding; 1.				
DR	ProDom; PD001115; 2Oxoacid dh; 1.				
DR	PROSITE; PS00189; LIPOYL; 1.				
KW	Glycolysis; Transferase; Acyltransferase; Lipoyl.				
FT	BINDING 42 42 LIPOYL (BY SIMILARITY).				
FT	ACT-SITE 411 411 POTENTIAL.				
SQ	SEQUENCE 438 AA; 46927 MW; 4BP83B697480B4B CRC64;				
Query Match	18.5%;	Score 114;	DB 1;	Length 438;	
Best Local Similarity	38.3%;	Pred. NO. 0.097;			
Matches	23;	Conservative 16;	Mismatches 21;	Indels 0;	Gaps 0;
QY	62	GTVSKVLKRGDTVFKAGQTVLVLEAMKMETEINAPTIDGKVKLVKRDVAVQGGQLIKI	121		
Db	16	GTVAEVLKVGVDVKEGSLFVEVDKNSBPAPVAGKIAPVAGIINIKAGQEIKVGVVMEI	75		
RESULT 35					
BCCP_HABIN		STANDARD;	PRT;	155 AA.	
ID	BCCP_HABIN				
AC	P43874;				
DT	01-NOV-1995 (Rel. 32, Created)				
DT	01-NOV-1995 (Rel. 32, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP).				
GN	ACCB OR FABB OR HI0971.				
OS	Haemophilus influenzae.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;				
OC	Pasteurellaceae; Haemophilus.				
OX	NCBI_TaxID=727;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Rd / KW20 / ATCC 51907;				
RX	MEDLINE=95350630; PubMed=7542800;				
RA	Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;				
RA	"Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";				
RT	Science 269:496-512 (1995).				
RL	[2]				
RN	SEQUENCE OF 1-10.				
RP	MEDLINE=20137488; PubMed=10675023;				
RX	Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B., Gray C., Fountoulakis M.;				
RA	"Two-dimensional map of the proteome of Haemophilus influenzae.";				
RL	Electrophoresis 21:411-429(2000).				
CC	-!- FUNCTION: This protein is a component of the acetyl coenzyme A carboxylase complex; first, biotin carboxylase catalyzes the carboxylation of the carrier protein and then the transcarboxylase transfers the carboxyl group to form malonyl-CoA (By similarity).				
CC	-!- PATHWAY: Long-chain fatty acid biosynthesis; first step.				
CC	-!- SUBUNIT: Homodimer (By similarity).				
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DR	EMBL; U32778; AAC22631.1; ..				
DR	Pf; E64105; E64105.				
DR	HSP; P02905; 1BDO.				
DR	TIGR; HI0971; ..				
DR	InterPro; IPR001249; AcCoA biotinCC.				
DR	InterPro; IPR001882; Biotin BS.				
DR	InterPro; IPR000089; Biotin lipoyl.				
DR	Pfam; PF00364; biotin lipoyl; 1.				
DR	PRINTS; PR01071; AC0ABIOTINCC.				
DR	TIGRFAMS; TIGR00531; BCCP; 1.				
DR	PROSITE; PS00188; BIOTIN; 1.				
KW	Fatty acid biosynthesis; Biotin; Complete proteome.				
FT	BINDING 121 121 BIOTIN (BY SIMILARITY).				
SQ	SEQUENCE 155 AA; 16247 MW; 696F19B4429A03CD CRC64;				
Query Match	18.2%;	Score 112;	DB 1;	Length 155;	
Best Local Similarity	31.2%;	Pred. NO. 0.053;			
Matches	30;	Conservative 16;	Mismatches 38;	Indels 12;	Gaps 2;

"Isolation of cDNA clones coding for the alpha and beta chains of human propionyl-CoA carboxylase: chromosomal assignments and DNA polymorphisms associated with PCCA and PCCB genes."; Proc. Natl. Acad. Sci. U.S.A. 83:4864-4868(1986). [6]

SEQUENCE OF 339-367 FROM N.A. TISSUE=Liver; MEDLINE=93167265; PubMed=8434582; Stankovics J., Ledley F.D.; "Cloning of functional alpha propionyl CoA carboxylase and correction of enzyme deficiency in PCCA fibroblasts."; Am. J. Hum. Genet. 52:144-151(1993). [7]

SEQUENCE OF 608-703 FROM N.A. MEDLINE=87212051; PubMed=3553348; Lamhonwah A.-M., Quan F., Gravel R.A.; "Sequence homology around the biotin-binding site of human propionyl-CoA carboxylase and pyruvate carboxylase."; Arch. Biochem. Biophys. 254:631-636(1987). [8]

REVIEW ON PA VARIANTS. MEDLINE=99433966; PubMed=10502773; Ugarte M., Perez-Cerda C., Rodriguez-Pombo P., Desviat L.R., Perez B., Richard E., Muro S., Campeau E., Ohura T., Gravel R.A.; "Overview of mutations in the PCCA and PCCB genes causing propionic acidemia."; Hum. Mutat. 14:275-282(1999). [9]

VARIANTS PA-1 TRP-52; THR-113; THR-139; LYS-348 AND ARG-606. MEDLINE=99203168; PubMed=1010253; Richard E., Desviat L.R., Perez B., Perez-Cerda C., Ugarte M.; "Genetic heterogeneity in propionic acidemia patients with alpha-subunit defects: identification of five novel mutations, one of them causing instability of the protein."; Biochim. Biophys. Acta 1453:351-358(1999). [10]

VARIANTS PA-1 PRO-50; LYS-204; GLY-343; VAL-354; ARG-643 AND CYS-687 DEL. MEDLINE=99263311; PubMed=10329019; Campeau E., Dupuis L., Leon-Del-Rio A., Gravel R.; "Coding sequence mutations in the alpha subunit of propionyl-CoA carboxylase in patients with propionic acidemia."; Mol. Genet. Metab. 67:11-22(1999).

-!- CATALYTIC ACTIVITY: ATP + propanoyl-CoA + HCO(3) (-) = ADP + phosphate + (S)-methylmalonyl-CoA.

-!- Cofactor: Biotin.

-!- PATHWAY: Key enzyme in the catabolic pathway of odd-chain fatty acids, isoleucine, threonine, methionine, and valine.

-!- SUBUNIT: Probably a dodecamer composed of six biotin-containing alpha subunits and six beta subunits.

-!- SUBCELLULAR LOCATION: Mitochondrial matrix.

-!- DISEASE: Defects in PCCA are the cause of propionic acidemia type I (PA-1) [MIM:606054]. PA-1 is a life-threatening disease characterized by episodic vomiting, lethargy and ketosis, neutropenia, periodic thrombocytopenia, hypogammaglobulinemia, developmental retardation, and intolerance to protein.

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EMBL: X14608; CAA32763.1; --  
EMBL: AY035808; AAK61392.1; JOINED.  
EMBL: AY035786; AAK61392.1; JOINED.  
EMBL: AY035787; AAK61392.1; JOINED.  
EMBL: AY035788; AAK61392.1; JOINED.  
EMBL: AY035789; AAK61392.1; JOINED.  
EMBL: AY035790; AAK61392.1; JOINED.  
EMBL: AY035791; AAK61392.1; JOINED.

DR EMBL; AY035792; AAK61392.1; JOINED.  
 DR EMBL; AY035793; AAK61392.1; JOINED.  
 DR EMBL; AY035794; AAK61392.1; JOINED.  
 DR EMBL; AY035795; AAK61392.1; JOINED.  
 DR EMBL; AY035796; AAK61392.1; JOINED.  
 DR EMBL; AY035797; AAK61392.1; JOINED.  
 DR EMBL; AY035798; AAK61392.1; JOINED.  
 DR EMBL; AY035799; AAK61392.1; JOINED.  
 DR EMBL; AY035800; AAK61392.1; JOINED.  
 DR EMBL; AY035801; AAK61392.1; JOINED.  
 DR EMBL; AY035802; AAK61392.1; JOINED.  
 DR EMBL; AY035803; AAK61392.1; JOINED.  
 DR EMBL; AY035804; AAK61392.1; JOINED.  
 DR EMBL; AY035805; AAK61392.1; JOINED.  
 DR EMBL; AY035806; AAK61392.1; JOINED.  
 DR EMBL; AY035807; AAK61392.1; JOINED.  
 DR EMBL; BC000140; AAK00140.1; -.  
 DR EMBL; M13572; AAA60035.1; -.  
 DR EMBL; S53656; AAB25345.1; -.  
 DR EMBL; M26121; AAA36424.1; -.  
 DR PIR; S04613; A27883.  
 DR HSSP; P24182; 1DV1.  
 DR Genew; HGNC:8653; PCCA.  
 DR GK; P05165; -.  
 DR MM; 232000; -.  
 DR MM; 606054; -.  
 DR GO; GO:0009374; F:biotin binding; TAS.  
 DR GO; GO:0004658; F:propionyl-CoA carboxylase activity; TAS.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR InterPro; IPR005482; Biotin\_Lipoyl.  
 DR InterPro; IPR000089; Biotin\_Lipoyl.  
 DR InterPro; IPR005479; Chase\_L\_D2.  
 DR InterPro; IPR005481; Chase\_L\_N.  
 DR Pfam; PF02785; Biotin\_carb\_C; 1.  
 DR Pfam; PF00364; biotin\_lipoyl; 1.  
 DR Pfam; PF020289; CPSase\_L\_chain; 1.  
 DR Pfam; PF02786; CPSase\_L\_D2; 1.  
 DR PROSITE; PS00188; Biotin; 1.  
 DR PROSITE; PS00866; CPSASE; 1.  
 DR PROSITE; PS00867; CPSASE2; 1.  
 DR Mitochondrion; Ligase; Biotin; ATP-binding; Transit peptide; Disease mutation; Polymorphism.  
 KW TRANSIT 1 20 MITOCHONDRION.  
 FT CHAIN 21 703 PROPIONYL-COA CARBOXYLASE ALPHA CHAIN.  
 FT NP\_BIND 198 203 ATP (POTENTIAL).  
 FT ACT\_SITE 328 328 BY SIMILARITY.  
 FT BINDING 669 669 BIOTIN (BY SIMILARITY).  
 FT VARIANT 50 50 A -> P (in PA-1).  
 FT VARIANT 52 52 R -> W (in PA-1).  
 FT VARIANT 113 113 A -> T (in PA-1).  
 FT VARIANT 139 139 I -> T (in PA-1).  
 FT VARIANT 204 204 M -> K (in PA-1).  
 FT VARIANT 272 272 Q -> R (in PA-1).  
 FT VARIANT 343 343 D -> G (in PA-1).  
 FT VARIANT 348 348 M -> K (in PA-1; unstable protein).  
 FT VARIANT 354 354 G -> V (in PA-1).  
 FT VARIANT 374 374 R -> Q (in PA-1).  
 Query Match 17.9%; Score 110; DB 1; Length 703;  
 Best Local Similarity 37.5%; Pred. No. 0.3;  
 Matches 24; Conservative 12; Mismatches 28; Indels 0; Gaps 0;

639 SMPGQVVAVSVKPGDAVAGQEI CVIEAMKQNSMTAGKTGTVKSVHCQAGSTVGEGLD 698  
 118 LIKI 121  
 699 LVEL 702  
 RESULT 37  
 BCCP\_CHLPN STANDARD; PRT; 167 AA.  
 ID BCCP\_CHLPN STANDARD; PRT; 167 AA.  
 AC Q9Z901;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP).  
 GN ACCB OR CPN0183 OR CP0585 OR CPB0186.  
 OS Chlamydia pneumoniae (Chlamydophila pneumoniae).  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.  
 OX NCBI\_TaxID=83558;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CWL029;  
 RX MEDLINE=99206606; PubMed=10192388;  
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,  
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;  
 RA "Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.";  
 RL Nat. Genet. 21:385-389(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AR39;  
 RX MEDLINE=20150255; PubMed=10684935;  
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heideberg J.F.,  
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,  
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,  
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,  
 RA Eisen J., Fraser C.M.;  
 RA "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia  
 pneumoniae AR39.";  
 RL Nucleic Acids Res. 28:1397-1406(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=J138;  
 RX MEDLINE=20330349; PubMed=10871362;  
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,  
 RA Shiba T., Iehii K., Hattori M., Kuhara S., Nakazawa T.;  
 RA "Comparison of whole genome sequences of Chlamydia pneumoniae J138  
 from Japan and CWL029 from USA.";  
 RL Nucleic Acids Res. 28:2311-2314(2000).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TW-183;  
 RA Geng M.M., Schuhmacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,  
 RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;  
 RA "The genome sequence of Chlamydia pneumoniae TW183 and comparison with  
 other Chlamydia strains based on whole genome sequence analysis.";  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: This protein is a component of the acetyl coenzyme A  
 carboxylase complex; first, biotin carboxylase catalyzes the  
 carboxylation of the carrier protein and then the transcarboxylase  
 transfers the carboxyl group to form malonyl-CoA (By similarity).  
 CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.  
 CC -!- SUBUNIT: Homodimer (By similarity).  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 DR EMBL; AE001604; AAL18336.1; -.  
 DR EMBL; AE002217; AAF38403.1; -.

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DR EMBL; AP002545; BAA989393.1; -
DR EMBL; AE017157; AAP98119.1; -
DR PIR; F72110; F72110.
DR PIR; G86513; G86513.
DR HSP; P02905; 3BDO.
DR PRC1-2DPAGE; Q92901; -.
DR TIGR; CP0585; -.
DR InterPro; IPR001249; AcCoA_biotinCC.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PRINTS; PR01071; ACOABIOCTINCC.
DR TIGRPFMs; TIGR00531; BCBP; 1.
DR PROSITE; PS00188; Biotin; Complete proteome.
KW fatty acid biosynthesis; Biotin; Complete proteome.
FT BINDING 129 129 BIOTIN (BY SIMILARITY).
SQ SEQUENCE 167 AA; 18461 MW; AAA1CF1801F9CE4C CRC64;

Query Match 17.6%; Score 108.5; DB 1; Length 167;
Best Local Similarity 38.4%; Pred. No. 0.1;
Matches 28; Conservative 9; Mismatches 29; Indels 7; Gaps 1;

QY 56 IPAPLAGTV-----SKLVKEGDTVKAGQTVLVLEAMKMETEINAPTQGVKVKLVKE 108
Db 90 ISSLVGVTFYSPAPDSFVFKPGDIVSEDTIVIVEAMKYNVEKAGMSRVLEVLITN 149

QY 109 RDAVQGGQGLIKI 121
Db 150 GDPVQFGSKLPRI 162

RESULT 39
ODO2 MYCTU STANDARD; PRT; 553 AA.
AC Q10381;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Dihydrolipoamide succinyltransferase component of 2-oxoglutarate
DE dehydrogenase complex (EC 2.3.1.61) (E2).
GN SUCH OR RV2215 OR MT2272 OR MTCY190.26 OR MB2238.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekoa F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skellton S., Squares R.,
RA Sultana J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White C.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Uitterback T., Weidman H., Khouri H., Gill J., Mikula A.,
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490(2002).

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RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.bovis; STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972;
RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
CC -!- FUNCTION: THE 2-OXOGLUTARATE DEHYDROGENASE COMPLEX CATALYZES THE
CC OVERALL CONVERSION OF 2-OXOGLUTARATE TO SUCCINYL-COA & CO(2). IT
CC CONTAINS MULTIPLE COPIES OF 3 ENZYMIC COMPONENTS: 2-OXOGLUTARATE
CC DEHYDROGENASE (E1), DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE (E2) AND
CC LIPOAMIDE DEHYDROGENASE (E3) (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Succinyl-CoA + dihydrolipoamide = CoA + S-
CC succinylidihydrolipoamide.
CC -!- COFACTOR: Contains 2 covalently bound lipoyl cofactors
CC (Potential).
CC -!- PATHWAY: Tricarboxylic acid cycle.
CC -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral
CC symmetry (By similarity).
CC -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z70283; CAA94256.1; -
CC EMBL; AE007072; AAK46557.1; -
CC EMBL; BX248341; CAD97091.1; -
CC PIR; H70786; H70786.
CC HSSP; P07016; 1C4T.
CC TIGR; MT2272; -.
CC TubercuList; RV2215; -.
CC InterPro; IPR001078; 2Oxoacid_dh.
CC InterPro; IPR000089; Biotin_lipoyl.
CC InterPro; IPR004167; E3_binding.
CC InterPro; IPR003016; Lipoyl_BS.
CC Pfam; PF00198; 2-oxoacid_dh_1.
CC Pfam; PF00364; biotin_lipoyl; 2.
CC Pfam; PF02817; e3_binding; 1.
CC PRODOM; PD00115; 2Oxoacid_dh; 1.
CC PROSITE; PS00189; Lipoyl; 2.
CC Tricarboxylic acid cycle; Transferase; Acyltransferase; Lipoyl;
CC Complete proteome.
CC BINDING 43 43 LIPOYL (POTENTIAL).
CC BINDING 162 162 LIPOYL (POTENTIAL).
CC ACT SITE 523 523 BY SIMILARITY.
CC ACT SITE 527 527 BY SIMILARITY.
CC SEQUENCE 553 AA; 57087 MW; 54B6E70D23B8047 CRC64;

Query Match 17.6%; Score 108; DB 1; Length 553;
Best Local Similarity 37.7%; Pred. No. 0.34;
Matches 23; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

QY 62 GTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQGVKVKLVKRDVQGGQGLIKI 121
Db 17 GTVTRWLKQEGDTVELDEPIVEVSTDKVDTEIPSPAAGVLTKIIAQEDDTVEVGGLAVI 76

QY 122 G 122
Db 77 G 77

RESULT 39
ID BTB7_MYCLE STANDARD; PRT; 70 AA.

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AC Q9CCH9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Biotinylated protein TB7.3 homolog.
GN ML0802.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RC MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eigmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mangall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RA "Massive gene decay in the leprosy bacillus.";
RT Nature 409:1007-1011 (2001).
RL -----
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CC or send an email to license@isb-sib.ch).
DR EMBL; AL583919; CAC30312.1; ALT_INIT.
DR HSSP; P10802; 11YU.
DR Leproma; ML0802; -.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; FALSE_NEG.
KW Biotin; Complete proteome.
FT INIT_MET 0 BY SIMILARITY.
FT BINDING 36 36 BIOTIN (BY SIMILARITY).
SQ SEQUENCE 70 AA; 7088 MW; B519F389DEF0447D CRC64;

Query Match 17.4%; Score 107; DB 1; Length 70;
Best Local Similarity 36.1%; Pred. No. 0.06;
Matches 22; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

QY 55 EIPAPLAGTISKILVKGDTVKAGQTVLVLEAMKMETEINAPTQKVKVLKRDVQV 114
Db 3 DVRAEIVASVLEVVVSEGDQIGKGVLLVLESMEKMEIPVLGAVGVSVSGVDVIOA 62

QY 115 G 115
Db 63 G 63

RESULT 40
ODP2_HAEN
ID_ODP2_HAEN STANDARD; PRT; 567 AA.
AC P45118;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase
DE complex (EC 2.3.1.12) (E2).
GN ACEF OR H11232.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RC MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
RA Rd.";
RL Science 269:496-512 (1995).
CC -!- FUNCTION: THE PYRUVATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL
CC CONVERSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAINS MULTIPLE
CC COPIES OF THREE ENZYMATIC COMPONENTS: PYRUVATE DEHYDROGENASE (E1),
CC DIHYDROLIPOAMIDE ACETYLTRANSFERASE (E2) & LIPOAMIDE DEHYDROGENASE
CC (E3) (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
CC acetyldihydrolipoamide.
CC -!- COFACTOR: Contains 2 covalently bound lipoyl cofactors (By
CC similarity).
CC -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral
CC symmetry (By similarity).
CC -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.
CC -----
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CC or send an email to license@isb-sib.ch).
DR EMBL; U32803; AAC22885.1; -.
DR PIR; I64111; I64111.
DR HSSP; P10802; 1DPC.
DR TIGR; H11232; -.
DR InterPro; IPR001078; 2Oxoacid_dh.
DR InterPro; IPR006256; AceF.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR004167; E3_binding.
DR InterPro; IPR003016; Lipoyl_BS.
DR Pfam; PF00198; 2-oxoacid_dh; 1.
DR Pfam; PF00364; biotin_lipoyl; 2.
DR Pfam; PF02817; e3_binding; 1.
DR PRODOM; PD001115; 2Oxoacid_dh; 1.
DR TIGRfams; TIGR01348; PDHac_trf_long; 1.
DR PROSITE; PS00189; LIPOYL; 2.
DR KW Glycolysis; Transferase; Acyltransferase; Repeat; Lipoyl;
KW Complete proteome.
FT DOMAIN 1 245 LIPOYL BINDING, ACIDIC.
FT DOMAIN 247 567 SUBUNIT BINDING, CATALYTIC.
FT BINDING 41 41 LIPOYL (BY SIMILARITY).
FT BINDING 147 147 LIPOYL (BY SIMILARITY).
FT ACT_SITE 484 484 POTENTIAL.
FT ACT_SITE 540 540 POTENTIAL.
FT ACT_SITE 544 544 POTENTIAL.
SQ SEQUENCE 567 AA; 59410 MW; 891DBDCBE388CSB0 CRC64;

Query Match 17.2%; Score 105.5; DB 1; Length 567;
Best Local Similarity 28.7%; Pred. No. 0.53;
Matches 39; Conservative 21; Mismatches 60; Indels 16; Gaps 4;

QY 1 MKLKVTVNGTAYDVVDV-DK-SHENPMGTILFGGGTGGAPAPAGAGAGAKA----- 51
Db 44 MEVPAEAGVVKKEILVKVGDKVSTGTGTPMLVLEAAGAPADEPTAPVADAPTAPVATAP 103
QY 52 ---GEGEIPAPLAG-----TVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVKV 104

```

Db 104 TASAIVENVDPDGGDEVNVEINVAVDITTEEQSLITVEGDKASMEVPAPPGGVKEI 163  
Qy 105 LVKERDAVQGGQGLIK 120  
Db 164 LVKSGDKVSTGSLIMR 179

Search completed: March 3, 2004, 10:29:43  
Job time : 13.7083 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 3, 2004, 10:26:14 ; Search time 10.2083 Seconds  
(without alignments)  
659.599 Million cell updates/sec

Title: US-09-987-485A-2

Perfect score: 342

Sequence: 1 EGEIPAPLAGTVSKILVKEG.....KVLVKERDAVQGGLIKIG 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:\*

1: Pir1.\*

2: Pir2.\*

3: Pir3.\*

4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	342	100.0	123	1 BKIP	biotin carboxyl ca
2	195	57.0	145	2 F75135	methymalonyl-coa
3	189	55.3	149	2 A71074	probable methylmal
4	180	52.6	571	2 F71133	probable oxaloacet
5	178	52.0	140	2 H69526	methymalonyl-CoA
6	174	50.9	655	2 B70432	pyruvate carboxyla
7	174	50.9	984	2 T44608	pyruvate carboxyla
8	173	50.6	567	2 F64453	oxaloacetate decar
9	170	49.7	186	2 D90418	hypothetical prote
10	167	48.8	134	2 C72341	propionyl-CoA carb
11	167	48.8	1144	2 D97227	pyruvate carboxyla
12	165	48.2	596	2 A28088	oxaloacetate decar
13	164	48.0	597	2 G82308	oxaloacetate decar
14	163	47.7	599	2 D81367	probable pyruvate
15	161	47.1	142	2 D69510	oxaloacetate decar
16	159.5	46.6	576	2 AC3038	biotin carboxylase
17	159.5	46.6	576	2 H98247	biotin carboxylase
18	159	46.5	665	2 G97819	hypothetical prote
19	158	46.2	607	2 F82966	probable transcarb
20	157	45.9	1146	2 AC1565	pyruvate carboxyla
21	157	45.9	1146	2 AH1208	pyruvate carboxyla
22	157	45.9	1150	2 AB3978	pyruvate carboxyla
23	153	44.7	620	2 F70439	oxaloacetate decar
24	152	44.4	167	2 T44291	biotin carboxyl ca
25	152	44.4	436	2 AS3568	methylocronoyl-Co
26	152	44.4	591	2 B44465	sodium ion pump ox
27	150	43.9	70	2 E81791	hypothetical prote
28	150	43.9	665	2 C71667	propionyl-CoA carb
29	148	43.3	591	2 AB0509	oxaloacetate decar

```

30 148 43.3 591 2 AE0909 oxaloacetate decar
31 148 43.3 1174 2 AE2911 pyruvate carboxyla
32 148 43.3 1174 2 C97886 pyruvate carboxyla
33 146 42.7 1150 2 G89881 pyruvate carboxyla
34 145 42.4 655 2 A83395 probable acyl-CoA
35 144 42.1 161 2 A95049 hypothetical prote
36 144 42.1 161 2 G97919 acetyl-CoA carboxy
37 143 41.8 730 2 G86161 hypothetical prote
38 143 41.8 1137 2 E86708 pyruvate carboxyla
39 143 41.8 1185 2 T39734 pyruvate carboxyla
40 142 41.5 155 2 H86721 hypothetical prote
41 141 41.2 1078 2 D87647 oxaloacetate decar
42 140 40.9 568 2 C69014 oxaloacetate decar
43 139.5 40.8 1127 2 D70671 pyruvate carboxyla
44 138.5 40.5 157 2 S73204 acetyl-CoA carboxy
45 138 40.4 129 2 D49094 methymalonyl-CoA

```

#### ALIGNMENTS

##### RESULT 1

BKIP

biotin carboxyl carrier protein [validated] - Propionibacterium freudenreichii subsp. s.  
N;Alternate names: methymalonyl-CoA carboxyltransferase biotin carboxyl carrier protei  
C;Species: propionibacterium freudenreichii subsp. shermanii  
C;Date: 31-Mar-1980 #sequence\_revision 31-Mar-1980 #text\_change 01-Feb-2002

C;Accession: A03401

R;Maloy, W.L.; Bowien, B.U.; Zwolinski, G.K.; Kumar, K.G.; Wood, H.G.; Ericsson, L.H.;

J. Biol. Chem. 254, 11615-11622, 1979

A;Title: Amino acid sequence of the biotinyl subunit from transcarboxylase.

A;Reference number: A03401; MUID:80049796; PMID:40985

A;Accession: A03401

A;Molecule type: protein

A;Residues: 1-123 <MAL>

C;Comment: Six or 12 chains of biotin carboxyl carrier protein (BCCP) are found in the  
onl coenzyme A to BCCP and (2) from BCCP to pyruvate, forming oxalacetate.

C;Comment: See PIR:A48665 and PIR:S36808.

C;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology

C;Keywords: biotin binding

F;50-123/Domain: lipoyl/biotin-binding homology <LFB>

F;89/Binding site: biotin (lys) (covalent) #status experimental

```

Query Match      100.0%; Score 342; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.le-27;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Cy 1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
    |||||
Db 54 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 113
    |||||

```

```

Cy 61 QGGGGLIKIG 70
    |||||
Db 114 QGGGGLIKIG 123

```

##### RESULT 2

F75135

methymalonyl-coa decarboxylase gamma chain PAB1771 - Pyrococcus abyssi (strain Orsay)

C;Species: Pyrococcus abyssi

C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000

C;Accession: F75135

R;anonymous; Genoscope

submitted to the EMBL Data Library, July 1999

A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str

A;Reference number: A75001

A;Accession: F75135

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-145 <KAW>

A;Cross-references: GB:AJ248285; GB:AL096836; NID:95458067; PIDN:CAB49799.1; PID:954583;

A;Experimental source: strain Orsay

C;Genetics:

C:Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/biotin

F:5/2-646/Domain: lipoyl/biotin-binding homology (Lys)  
F:672/Binding site: biotin (Lys) #status predicted





D69510  
oxaloacetate decarboxylase, biotin carboxyl carrier subunit homolog - Archaeoglobus fulgidus  
C/Species: Archaeoglobus fulgidus  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Aug-1999  
C/Accession: D69510  
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A/Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo  
A/Reference number: A69250; MUID:98049343; PMID:9389475  
A/Accession: D69510  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-142 <KLE>  
A/Cross-references: GB:AE000960; GB:AE000782; NID:92699283; PIDN:AA89171.1; PID:g264844  
C/Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology  
F;66-139/Domain: lipoyl/biotin-binding homology <LPB>

Query Match 47.1%; Score 161; DB 2; Length 142;  
Best Local Similarity 50.8%; Pred. No. 3.6e-09;  
Matches 32; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVLKRDVAV 60  
Db 70 ENAVTSMPLPGVVLKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVLKRDVAV 60

QY 61 QGGGLIKI 69  
Db 130 QAGATLIDI 574

RESULT 16  
AC3038  
biotin carboxylase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C/Species: Agrobacterium tumefaciens  
C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
C/Accession: AC3038  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A/Reference number: AB2577; MUID:21608550; PMID:11743193  
A/Accession: AC3038  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-576 <KUR>  
A/Cross-references: GB:AE008689; PIDN:AA444721.1; PID:gl7742353; GSPDB:GN00187  
A/Experimental source: strain C58 (Dupont)  
C/Genetics:

Query Match 46.6%; Score 159.5; DB 2; Length 576;  
Best Local Similarity 50.7%; Pred. No. 2.2e-08;  
Matches 35; Conservative 13; Mismatches 20; Indels 1; Gaps 1;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVLKRDVAV 60  
Db 507 EGEIMPVSGTLQSFVKDGETVSEGLLAVMEAMKMETQIVATRAGKV-RLIVKEGDYL 565

QY 61 QGGGLIKI 69  
Db 566 QAGATLIDI 574

RESULT 17  
AC3038  
biotin carboxylase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C/Species: Agrobacterium tumefaciens  
C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
C/Accession: AC3038  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A/Reference number: AB2577; MUID:21608550; PMID:11743193  
A/Accession: AC3038  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-576 <KUR>  
A/Cross-references: GB:AE008689; PIDN:AA444721.1; PID:gl7742353; GSPDB:GN00187  
A/Experimental source: strain C58 (Dupont)  
C/Genetics:

Query Match 46.6%; Score 159.5; DB 2; Length 576;  
Best Local Similarity 50.7%; Pred. No. 2.2e-08;  
Matches 35; Conservative 13; Mismatches 20; Indels 1; Gaps 1;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVLKRDVAV 60  
Db 507 EGEIMPVSGTLQSFVKDGETVSEGLLAVMEAMKMETQIVATRAGKV-RLIVKEGDYL 565

QY 61 QGGGLIKI 69  
Db 566 QAGATLIDI 574

RESULT 17

H98247  
biotin carboxylase protein A2 [imported] - Agrobacterium tumefaciens (strain C58, Cereoi  
C/Species: Agrobacterium tumefaciens  
C/Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 18-Nov-2002  
C/Accession: H98247  
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman  
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.  
Science 294, 2323-2328, 2001  
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu  
A/Reference number: A97359; MUID:21608551; PMID:11743194  
A/Accession: H98247  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-576 <KUR>  
A/Cross-references: GB:AE007870; PIDN:AAK89506.1; PID:gl5159380; GSPDB:GN00170  
C/Genetics:

Query Match 46.6%; Score 159.5; DB 2; Length 576;  
Best Local Similarity 50.7%; Pred. No. 2.2e-08;  
Matches 35; Conservative 13; Mismatches 20; Indels 1; Gaps 1;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVLKRDVAV 60  
Db 507 EGEIMPVSGTLQSFVKDGETVSEGLLAVMEAMKMETQIVATRAGKV-RLIVKEGDYL 565

QY 61 QGGGLIKI 69  
Db 566 QAGATLIDI 574

RESULT 18  
G97819  
hypothetical protein pcca [imported] - Rickettsia conorii (strain Malish 7)  
C/Species: Rickettsia conorii  
C/Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 22-Oct-2001  
C/Accession: G97819  
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ri  
Science 293, 2093-2098, 2001  
A/Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.  
A/Reference number: A97700; MUID:21442074; PMID:11557893  
A/Accession: G97819  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-665 <KUR>  
A/Cross-references: GB:AE006914; PIDN:AA403497.1; PID:gl5620071; GSPDB:GN00173  
C/Genetics:

Query Match 46.5%; Score 159; DB 2; Length 665;  
Best Local Similarity 50.0%; Pred. No. 2.8e-08;  
Matches 33; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 3 EIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVLKRDVAV 62  
Db 598 ELQAPLGGQIAIKVKGQEVTAQGEIMILTAMKWNILIAERDGTAKIAFVNEKDVIR 657

QY 63 QGGGLIK 68  
Db 658 QGVLE 663

RESULT 19  
F82966  
probable transcarboxylase subunit PA5435 [imported] - Pseudomonas aeruginosa (strain PA  
C/Species: Pseudomonas aeruginosa  
C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C/Accession: F82966  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bi  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

```

.: Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F82966
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-607 <STO>
A;Cross-references: GB:AE004956; GB:AE004091; MID:g9951760; PIDN:AAG08820.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA5435
C;Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/biotin-binding

Query Match 46.2%; Score 158; DB 2; Length 607;
Best Local Similarity 48.5%; Pred. No. 3.2e-08;
Matches 33; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

QY 2 GEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVVKERDAVQ 61
Db 538 GHVSTMPGNIVDLVKEGDSVAGQAVLITEAMKMETEQVQAGIAGTVKRAIHVAKGRVN 597

QY 62 GQGLIKI 69
Db 598 PGEILIEI 605

RESULT 20
AC1565
pyruvate carboxylase homolog pyca [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AC1565
R;Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.: Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlant
A;Title: Comparative Genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1565
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1146 <GLA>
A;Cross-references: GB:AL502022; PIDN:CAC96291.1; PID:g16413519; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: pyca
C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding

Query Match 45.9%; Score 157; DB 2; Length 1146;
Best Local Similarity 43.3%; Pred. No. 7.9e-08;
Matches 29; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

QY 4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVVKERDAVQGG 63
Db 1078 VGATMGSVIQVVKGDSVKKGDPPLITEAMKMETTIQAPFDGEVSSIVSDGTIESG 1137

QY 64 QGLIKI 69
Db 1138 DLLIEV 1143

RESULT 21
AH1208
pyruvate carboxylase homolog pyca [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AH1208
R;Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.: Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.

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Science 294, 849-852, 2001
A;Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlant
A;Title: Comparative Genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1208
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1146 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC99150.1; PID:g16410474; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: pyca
C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding

Query Match 45.9%; Score 157; DB 2; Length 1146;
Best Local Similarity 43.9%; Pred. No. 7.9e-08;
Matches 29; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

QY 4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVVKERDAVQGG 63
Db 1078 VGATMGSVIQVVKGDSVKKGDPPLITEAMKMETTIQAPFDGEVSSIVSDGTIESG 1137

QY 64 QGLIKI 69
Db 1138 DLLIEV 1143

RESULT 22
AB3978
pyruvate carboxylase pyca [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: AB3978
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans an
A;Reference number: AB3650; MUID:20512582; PMID:11058132
A;Accession: AB3978
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1150 <STO>
A;Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06344.1; GSPDB:GN
A;Experimental source: strain C-125
C;Genetics:
A;Gene: pyca
C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding

Query Match 45.9%; Score 157; DB 2; Length 1150;
Best Local Similarity 50.0%; Pred. No. 7.9e-08;
Matches 33; Conservative 13; Mismatches 20; Indels 0; Gaps 0;

QY 4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVVKERDAVQGG 63
Db 1082 IGASMPGTIVKALVEKGVKQGDHLMITEAMKMETTVQAPFDGEVVALHVKGDAIQTG 1141

QY 64 QGLIKI 69
Db 1142 DLLIEV 1147

RESULT 23
F70439
oxaloacetate decarboxylase alpha chain - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 18-Aug-2000
C;Accession: F70439
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; C
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: F70439

```







A;Experimental source: strain C58 (Dupont)  
 C;Genetics:  
 A;Gene: pyca  
 A;Map position: circular chromosome  
 C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding

Query Match 43.3%; Score 148; DB 2; Length 1174;  
 Best Local Similarity 45.3%; Pred. No. 6.5e-07;  
 Matches 29; Conservative 13; Mismatches 22; Indels 0; Gaps 0;

QY 4 IPAPLAGTGVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVLYKRDVAVGG 63  
 DB 1107 IGAPMPGVISRVFINGQGVKAGDVLISIEAMKMETALHAERDGGKIAEVLVVKPGDQIDAK 1166

QY 64 QGLI 67  
 DB 1167 DLLI 1170

RESULT 32  
 C97686  
 Pyruvate carboxylase (U51439) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)  
 C;Species: Agrobacterium tumefaciens  
 C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002  
 C;Accession: C97686  
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, M.; Blanchard, M.; Ourullo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001  
 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens  
 A;Reference number: A97359; MUID:21608551; PMID:11743194  
 A;Accession: C97686  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-1174 <KUR>  
 A;Cross-references: GB:AE007869; PIDN:AAK98444.1; PID:gl5157941; GSPDB:GN00169  
 C;Genetics:  
 A;Gene: AGR\_C 4940  
 A;Map position: circular chromosome  
 C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding

Query Match 43.3%; Score 148; DB 2; Length 1174;  
 Best Local Similarity 45.3%; Pred. No. 6.5e-07;  
 Matches 29; Conservative 13; Mismatches 22; Indels 0; Gaps 0;

QY 4 IPAPLAGTGVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVLYKRDVAVGG 63  
 DB 1107 IGAPMPGVISRVFINGQGVKAGDVLISIEAMKMETALHAERDGGKIAEVLVVKPGDQIDAK 1166

QY 64 QGLI 67  
 DB 1167 DLLI 1170

RESULT 33  
 G99881  
 pyruvate carboxylase [imported] - Staphylococcus aureus (strain N315)  
 C;Species: Staphylococcus aureus  
 C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001  
 C;Accession: G99881  
 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayaishi, H.; Hiramatsu, K.; Lancet 357, 1225-1240, 2001  
 A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
 A;Reference number: A89758; MUID:21311952; PMID:11418146  
 A;Accession: G99881  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-1150 <KUR>  
 A;Cross-references: GB:BA000018; PID:gl3700915; PIDN:BA842211.1; GSPDB:GN00149  
 A;Experimental source: strain N315  
 C;Genetics:  
 A;Gene: PYCA

C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding

Query Match 42.7%; Score 146; DB 2; Length 1150;  
 Best Local Similarity 47.0%; Pred. No. 1e-06;  
 Matches 31; Conservative 13; Mismatches 22; Indels 0; Gaps 0;

QY 4 IPAPLAGTGVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVLYKRDVAVGG 63  
 DB 1080 IGAPMPGVISRVFINGQGVKAGDVLISIEAMKMETIQAFFDGVKIQVTNNNGDTIATG 1139

QY 64 QGLI 69  
 DB 1140 DLLIEI 1145

RESULT 34  
 A83395  
 probable acyl-CoA carboxylase alpha chain PA2012 [imported] - Pseudomonas aeruginosa (s)  
 C;Species: Pseudomonas aeruginosa  
 C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C;Accession: A83395  
 R;Stover, C.K.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim adman, S.; Lory, S.; Olson, M.V.; Nature 406, 959-964, 2000  
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.  
 A;Reference number: A82950; MUID:20437337; PMID:10984043  
 A;Accession: A83395  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-655 <STO>  
 A;Cross-references: GB:AE004627; GB:AE004091; NID:G9948007; PIDN:AAG05400.1; GSPDB:GN00  
 A;Experimental source: strain PAO1  
 C;Genetics:  
 A;Gene: PA2012  
 C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipo

Query Match 42.4%; Score 145; DB 2; Length 655;  
 Best Local Similarity 42.0%; Pred. No. 7.1e-07;  
 Matches 29; Conservative 18; Mismatches 22; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTGVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVLYKRDVAV 60  
 DB 582 QGGLSPMNGSIVRVLPVGQTVGAGATLVVLEAMKMEHSIRAPHAGVVKALYCSGELV 641

QY 61 QGGQGLIKI 59  
 DB 642 BEGTPLVEL 650

RESULT 35  
 A95049  
 hypothetical protein SP0423 [imported] - Streptococcus pneumoniae (strain TIGR4)  
 C;Species: Streptococcus pneumoniae  
 C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 24-Aug-2001  
 C;Accession: A95049  
 R;Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.; Science 293, 498-506, 2001  
 A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
 A;Reference number: A95000; MUID:21357209; PMID:11463916  
 A;Accession: A95049  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-161 <KUR>  
 A;Cross-references: GB:AE005672; PIDN:AAK74586.1; PID:gl14971893; GSPDB:GN00164; TIGR:SP  
 A;Experimental source: strain TIGR4  
 C;Genetics:  
 A;Gene: SP0423  
 C;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology

Query Match 42.1%; Score 144; DB 2; Length 161;  
Best Local Similarity 41.6%; Pred. No. 2.1e-07;  
Matches 32; Conservative 15; Mismatches 22; Indels 8; Gaps 2;

QY 1 EGE-IPAPLAGTV-----SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKV 52  
DB 84 EGNLVESPLGVVYLAAGPKPAFTVGVDSVKKGQTLVILEAMKVMNEIPAPKGVVTEI 143

QY 53 LVKERDAVQGGGLIKI 69  
DB 144 LVSNEEMVFGKGLVRI 160

RESULT 36  
G97919  
acetyl-CoA carboxylase (EC 6.4.1.2), carboxyltransferase beta chain [imported] - Streptococcus pneumoniae  
C;Species: Streptococcus pneumoniae  
C;Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 02-Nov-2001  
C;Accession: G97919  
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczyk, L.; Burgett, S.; DeHoff, B.S.; Eick, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Meyer, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; et al.  
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A;Reference number: A97872; MUID:21429245; PMID:111544234  
A;Accession: G97919  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-161 <KUR>  
A;Cross-references: GB:AE007317; PIDN:AAK99187.1; PID:g15457944; GSPDB:GN00174  
C;Genetics:  
A;Gene: accB  
A;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology  
C;Keywords: ligase

Query Match 42.1%; Score 144; DB 2; Length 161;  
Best Local Similarity 41.6%; Pred. No. 2.1e-07;  
Matches 32; Conservative 15; Mismatches 22; Indels 8; Gaps 2;

QY 1 EGE-IPAPLAGTV-----SKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKV 52  
DB 84 EGNLVESPLGVVYLAAGPKPAFTVGVDSVKKGQTLVILEAMKVMNEIPAPKGVVTEI 143

QY 53 LVKERDAVQGGGLIKI 69  
DB 144 LVSNEEMVFGKGLVRI 160

RESULT 37  
G86161  
hypothetical protein F103.9 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2001  
C;Accession: G86161  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chao, M.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; et al.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; et al.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: G86161  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-730 <STO>  
A;Cross-references: GB:AE005172; NID:g4587569; PIDN:AAD25800.1; GSPDB:GN00141  
C;Genetics:  
A;Map position: 1

C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoyl/

Query Match 41.8%; Score 143; DB 2; Length 730;  
Best Local Similarity 45.6%; Pred. No. 1.3e-06;  
Matches 31; Conservative 10; Mismatches 27; Indels 0; Gaps 0;

QY 2 GRIPPLAGTGVKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLEKRDVAVQ 61  
DB 661 GTIVAPMAGLVVVKLVLEAKYDQGPILVLEAMKMEHVVKAPSSGSIQDLVKVAGQQVYS 720

QY 62 GQGGLIKI 69  
DB 721 DGSALFRI 728

RESULT 38  
E86708  
pyruvate carboxylase (EC 6.4.1.1) [imported] - Lactococcus lactis subsp. lactis (strain C;Species: Lactococcus lactis subsp. lactis  
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
C;Accession: E86708  
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrlich, S.; et al.  
Genome Res. 11, 731-753, 2001  
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis : A;Reference number: A86625; MUID:21235186; PMID:11337471  
A;Accession: E86708  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1137 <STO>  
A;Cross-references: GB:AE005176; PID:g12723576; PIDN:AAK04767.1; GSPDB:GN00146  
A;Experimental source: strain IL1403  
C;Genetics:  
A;Gene: pyCA  
A;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding  
C;Keywords: ligase

Query Match 41.8%; Score 143; DB 2; Length 1137;  
Best Local Similarity 47.8%; Pred. No. 2e-06;  
Matches 32; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

QY 3 EIPAPLAGTGVKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLEKRDVAVQ 62  
DB 1070 QICATWPGSVLEILVKAGDKVQKQALMVTAMKMETTIEAPDPDGEIVDLHVVKGEAIQT 1129

QY 63 GQGGLIKI 69  
DB 1130 QDLLEI 1136

RESULT 39  
T39734  
pyruvate carboxylase (EC 6.4.1.1) [similarity] - fission yeast (Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 11-Jan-2002  
C;Accession: T39734; T42534  
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.  
submitted to the EMBL Data Library, August 1999  
A;Reference number: Z21874  
A;Accession: T39734  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-1185 <WOO>  
A;Cross-references: EMBL:AL109846; PIDN:CAB52809.1; GSPDB:GN00067; SPDB:SPBC17G9.11C  
A;Experimental source: strain 972h(-); cosmid cl799  
R;Saito, A.; Kazuta, Y.; Toh, H.; Kondo, H.; Tanabe, T.  
submitted to the EMBL Data Library, October 1995  
A;Description: Biotin-dependent enzymes in Schizosaccharomyces pombe: cloning and nucleic acid  
A;Reference number: Z22172  
A;Accession: T42534  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-67, 17, 69-1185 <SAI>  
A;Cross-references: EMBL:D78170; PIDN:BAAL1239.1

Search completed: March 3, 2004, 10:31:49  
Job time : 11.2083 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 3, 2004, 10:25:29 ; Search time 45.1146 Seconds  
(without alignments) 853.232 Million cell updates

Title: US-09-987-485A-1  
Perfect score: 615  
Sequence: 1 MKIKVTNGTAYDVPDVK.....KVLNKEPDAVGGGGLIKG 122

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

```

```
Database :
SPRENMBL.25.*
1:  sp_arched.*
2:  sp_bacteria.*
3:  sp_fungi.*
4:  sp_human.*
5:  sp_invertebrate.*
6:  sp_mammal.*
7:  sp_mhc.*
8:  sp_organelle.*
9:  sp_phase.*
10: sp_plant.*
11: sp_prodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	286	46.5	120	16	Q8FRF4	Q8frf4	corynebacte
2	231.5	37.6	145	17	Q9V0A6	Q9v0a6	pyrococcus
3	221	35.9	149	17	O59021	O59021	pyrococcus
4	216	35.4	144	17	Q8U303	Q8u303	pyrococcus
5	205	33.3	129	2	Q57111	Q57111	vellonella
6	198.5	32.3	134	2	O54030	O54030	propionigen
7	196.5	32.0	145	2	Q9ZAA7	Q9zaa7	acidaminoco
8	190.5	31.0	655	16	O67484	O67484	auquifex aeo
9	190	30.9	140	17	O28067	O28067	archaeoglob
10	188	30.6	116	16	Q99ZL6	Q99zl6	streptococc
11	187.5	30.5	599	16	Q3PP00	Q3pp00	campylobact
12	187	30.4	116	16	Q8K7G1	Q8k7g1	streptococc
13	186	30.2	116	16	Q8P104	Q8p104	streptococc
14	185	30.1	144	16	Q8A737	Q8a737	bacteroides
15	185	30.1	597	16	Q9KUH1	Q9kuh1	vibrio chol
16	185	30.1	986	16	O891V8	O891v8	clostridium

17	184	29.9	571	17	Q58564	O58564	pyrococcus
18	179.5	29.2	122	16	Q87M0	Q87M0	thermoanaer
19	176.5	28.7	576	16	Q8U917	Q8U917	agrobacteri
20	176	28.6	134	16	Q9WZH6	Q9WZH6	thermotoga
21	176	28.6	596	2	Q49826	Q49826	legionella
22	176	28.6	984	2	Q9XBJ1	Q9XBJ1	bacillus ce
23	176	28.6	1148	16	Q819M9	Q819M9	bacillus ce
24	175.5	28.5	133	16	Q82V7	Q82V7	enterococu
25	175.5	28.5	602	16	Q8BC37	Q8BC37	pseudomonas
26	175.5	28.5	610	17	Q9HP38	Q9HP38	halobacteri
27	175	28.5	1148	16	Q81MT6	Q81MT6	bacillus an
28	174	28.5	456	16	Q8FRP0	Q8FRP0	corynebacte
29	174	28.3	591	2	Q8Q2N4	Q8Q2N4	corynebacte
30	173.5	28.2	131	16	Q8K7F5	Q8K7F5	streptococc
31	173.5	28.2	132	16	Q99ZL1	Q99ZL1	streptococc
32	173.5	28.2	186	17	Q97VY7	Q97VY7	sulfolobus
33	173.5	28.2	591	16	Q8XGX8	Q8XGX8	salmonella
34	172.5	28.0	602	16	Q87U07	Q87U07	pseudomonas
35	172	28.0	114	16	Q8R5Y8	Q8R5Y8	thermoanaer
36	171.5	27.9	1144	16	Q88VC5	Q88VC5	lactobacill
37	171	27.8	595	16	Q87L7R	Q87L7R	vibrio para
38	170.5	27.7	591	16	P71122	P71122	corynebacte
39	170.5	27.7	596	16	Q8DC43	Q8DC43	vibrio vuln
40	170	27.6	1144	16	Q97F7R	Q97F7R	clostridium
41	169.5	27.6	111	16	Q8P0Z8	Q8P0Z8	streptococc
42	168.5	27.4	607	16	Q9HTD1	Q9HTD1	pseudomonas
43	168.5	27.4	620	16	Q67544	Q67544	aquifex ae
44	168	27.3	135	16	Q9RAJ2	Q9RAJ2	thermoanaer
45	168	27.3	158	16	Q92OK0	Q92OK0	rhizobium m

## ALIGNMENTS

## RESULT 1

```

ID      Q8FRF4      PRELIMINARY;      PRY;      120 AA.
AC
Q8FRF4;
DT      01-MAR-2003 (TREMBlrel. 23, Created)
DT      01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT      01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE      Putative biotin carboxyl carrier protein.
GN      C08007.
OS      Corynebacterium efficiens.
OC      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC      Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX      NCBI_TaxID=152794;
[1]
RN      SEQUENCE FROM N.A.
RC      STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA      Kawarabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA      Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA      Usuda Y., Sugimoto S.;
RA      "The entire genomic sequence of Corynebacterium efficiens YS-314." ;
RT      Submitted (MAY-2002) to the EMBL/GenBank/DBSJ databases.
RL      EMBL; AF005216; BAC17617.1; -.
RL      GO; GO:000374; F:biotin binding; IEA.
DR      InterPro; IPR001882; Biotin BS.
DR      InterPro; IPR000089; Biotin_lipoyl.
DR      Pfam; PF00364; biotin_lipoyl; 1.
DR      PROSITE; PS00188; BIOTIN; 1.
DR      Complete proteome.
KW      SEQUENCE 120 AA; 12298 MW; 4C36E4AB41C969E5 CRC64;

```

Query Match	46.5%	Score	286;	DB	16;	Length	120;
Best Local Similarity	52.9%	Pred. No.	5.1e-16;				
Matches	64;	Conservative	19;	Mismatches	37;	Indels	2;
Gaps	2;						

  

Qy	1	M	K	L	V	T	V	N	G	T	A	Y	D	V	D	V	D	K	S	H	E	N	P	M	T	I	L	L	G	G	T	G	G	A	P	A	P	A	G	A	G	A	G	A	G	E	E	I	P	A	L	60
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:
Db	1	M	K	L	N	V	T	G	I	N	T	Y	N	E	V	E	E	-	E	Q	R	L	G	P	I	I	I	G	S	A	R	T	N	P	A	P	T	A	S	I	Q	G	V	A	N	A	-	V	V	A	L	58

  

Qv	61	A	G	T	V	S	K	I	L	R	E	G	D	T	V	K	A	G	Q	T	V	L	E	A	M	K	M	E	T	E	N	A	P	T	D	G	K	V	L	V	K	R	D	A	V	Q	G	G	L	I	K	120
----	----	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	-----

```
Db 59 AGSVKILVAGDTTIRAGQVLIVLEANKMETITAPSAGVGVAINVKEAGEVQGGSLIE 118
QY 121 I 121
Db 119 I 119

RESULT 2
Q9V0A6 PRELIMINARY; PRT; 145 AA.
ID Q9V0A6
AC Q9V0A6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Methylmalonyl-CoA decarboxylase gamma chain.
GN PYRAB08850 OR PAB1771.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae;
OC Pyrococcus
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GES / Orsay;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; A248285; CAB49799.1; -.
DR FIR; F75135; F75135.
DR HSSP; P02905; LBDO.
DR GO; GO:0009374; F:biotin binding; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Complete proteome.
SQ SEQUENCE 145 AA; 15489 MW; 9C14433663F40D94 CRC64;

Query Match 37.6%; Score 231.5; DB 17; Length 145;
Best Local Similarity 41.4%; Pred. No. 1.8e-11;
Matches 60; Conservative 18; Mismatches 44; Indels 23; Gaps 3;

QY 1 MKLKVTVNGTAYDVIDV-----VDKSHE-----NPMGTILFGGGTGADA 40
Db 1 MKKVTVNGKEYEVDVEVMPGKFRVLTGKTYEVEANLGIQVAPQTQVATPPTPT 60

QY 41 PA---AGGAGAGAGAGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPT 97
Db 61 PTPVQAPTTPQVQASENVVTPMPGKVLKILVQGGQVQKLGGLLILEAMKMETEINAPT 120

QY 98 DGKVEKVLKERDAVQGGGLIKIG 122
Db 121 DGVVKKILVAGDAVDGTGTLEILG 145

RESULT 3
O59021 PRELIMINARY; PRT; 149 AA.
ID O59021
AC O59021;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 149AA long hypothetical methylmalonyl-CoA decarboxylase gamma chain.
GN PH1284.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae;
OC Pyrococcus
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
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RA Kwarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
DR EMBL; AF000005; BAA30387.1; -.
DR FIR; A71074; A71074.
DR HSSP; P10802; LIYU.
DR GO; GO:0009374; F:biotin binding; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Complete proteome.
SQ SEQUENCE 149 AA; 15985 MW; 1C3AAS4F7B6BA6F1 CRC64;

Query Match 35.9%; Score 221; DB 17; Length 149;
Best Local Similarity 36.3%; Pred. No. 1.3e-10;
Matches 53; Conservative 21; Mismatches 48; Indels 24; Gaps 1;

QY 1 MKLKVTVNGTAYDVIDV-----VDKSHENPMGTILFGGGTG 36
Db 4 MKKVTVNGKEYEVDVEVMPGKFRVLTGKTYEVEVTSAGFVTSKQVQVTPAPTAPA 63

QY 37 GAPAPAGAGAGAGAGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAP 96
Db 64 PTPTPAPAPSSKTVSVSNVVSAPMPGKVLRLVLRVGDVRVQGGLLVLEAMKMETEINAP 123

QY 97 TDGKVEKVLKERDAVQGGGLIKIG 122
Db 124 RGVVKKILVKEGEAVDTGQPLIELG 149

RESULT 4
O8U303 PRELIMINARY; PRT; 144 AA.
ID O8U303
AC O8U303;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Methylmalonyl-CoA decarboxylase gamma chain.
GN PF0673.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010188; AAL80797.1; -.
DR GO; GO:0009374; F:biotin binding; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Complete proteome.
SQ SEQUENCE 144 AA; 15315 MW; 422C96A8ED809C6A CRC64;

Query Match 35.4%; Score 218; DB 17; Length 144;
Best Local Similarity 36.7%; Pred. No. 2.2e-10;
Matches 54; Conservative 21; Mismatches 44; Indels 28; Gaps 3;

QY 1 MKLKVTVNGTAYDVIDV-----VDKSHENPMGTILFGGGTGGA 38
Db 1 MKKVINGEEVEVEEIMPCKVLTGKTYEVEAKDLGISTPAPVQV---PTPTPA 57
```

QY 39 PAPA---AGGAGKAGEGEIPAPLAGTAVSKILVKEGDTKAGQTVLVLEAMKMETEINA 95  
 DB 58 PAPAPMPTSPASQVGDVNTVTPMPGKILKILVSEGQRTVIGQGLILEAMKMEINEIPS 117  
 QY 96 PTQGVKEVLVKERDAVQGGQGLIKIG 122  
 DB 118 PKDGVKKIYVKEGDTVDTCQPLIELG 144

## RESULT 5

Q57111 PRELIMINARY; PRT; 129 AA.  
 AC Q57111;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Gamma-subunit, methylmalonyl-CoA decarboxylase.  
 OS Veillonella parvula.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Acidaminococcaceae;  
 OC Veillonella.  
 CX NCBI\_TaxID=29466;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Huder J.B., Dimroth P.;  
 RA J. Biol. Chem. 0:0-0(1993).  
 RN [2]

QY 39 PAPA---AGGAGKAGEGEIPAPLAGTAVSKILVKEGDTKAGQTVLVLEAMKMETEINA 95  
 DB 58 PAPAPMPTSPASQVGDVNTVTPMPGKILKILVSEGQRTVIGQGLILEAMKMEINEIPS 117  
 QY 96 PTQGVKEVLVKERDAVQGGQGLIKIG 122  
 DB 118 PKDGVKKIYVKEGDTVDTCQPLIELG 144

QY 39 PAPA---AGGAGKAGEGEIPAPLAGTAVSKILVKEGDTKAGQTVLVLEAMKMETEINA 95  
 DB 58 PAPAPMPTSPASQVGDVNTVTPMPGKILKILVSEGQRTVIGQGLILEAMKMEINEIPS 117  
 QY 96 PTQGVKEVLVKERDAVQGGQGLIKIG 122  
 DB 118 PKDGVKKIYVKEGDTVDTCQPLIELG 144

QY 39 PAPA---AGGAGKAGEGEIPAPLAGTAVSKILVKEGDTKAGQTVLVLEAMKMETEINA 95  
 DB 58 PAPAPMPTSPASQVGDVNTVTPMPGKILKILVSEGQRTVIGQGLILEAMKMEINEIPS 117  
 QY 96 PTQGVKEVLVKERDAVQGGQGLIKIG 122  
 DB 118 PKDGVKKIYVKEGDTVDTCQPLIELG 144

QY 39 PAPA---AGGAGKAGEGEIPAPLAGTAVSKILVKEGDTKAGQTVLVLEAMKMETEINA 95  
 DB 58 PAPAPMPTSPASQVGDVNTVTPMPGKILKILVSEGQRTVIGQGLILEAMKMEINEIPS 117  
 QY 96 PTQGVKEVLVKERDAVQGGQGLIKIG 122  
 DB 118 PKDGVKKIYVKEGDTVDTCQPLIELG 144

## RESULT 6

O54030 PRELIMINARY; PRT; 134 AA.  
 AC O54030;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Methylmalonyl-CoA decarboxylase, gamma-subunit (EC 4.1.1.41).  
 GN MMDc.  
 OS Propionigenium modestum.  
 OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;

OC Propionigenium.  
 CX NCBI\_TaxID=2333;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DSM 2376;  
 RX MEDLINE=9808990; PubMed=9428714;  
 RA Bott M., Pfister K., Burda P., Kalbermatter O., Woelke G.,  
 RA Dimroth P.;  
 RT "Methylmalonyl-CoA decarboxylase from Propionigenium modestum: Cloning  
 and sequencing of the structural genes and purification of the enzyme  
 complex";  
 RL Eur. J. Biochem. 250:590-599(1997).  
 CC -I- COFACTOR: BIOTIN (BY SIMILARITY).  
 DR EMBL; AJ002015; CAA05139.1; -;  
 DR PIR; T44984; T44984.  
 DR HSSP; P02905; 1BD0.  
 DR GO; GO:0009374; F:biotin binding; IEA.  
 DR GO; GO:0016829; F:lyase activity; IEA.  
 DR GO; GO:0004492; F:methylmalonyl-CoA decarboxylase activity; IEA.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR Pfam; PF00364; biotin\_lipoyl; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 DR Biotin; Lyase.  
 KW Biotin; Lyase.  
 SQ SEQUENCE 134 AA; 13094 MW; 72CC813187273873 CRC64;

Query Match 32.3%; Score 198.5; DB 2; Length 134;  
 Best Local Similarity 38.5%; Pred. No. 8e-09;  
 Matches 52; Conservative 12; Mismatches 44; Indels 27; Gaps 3;  
 QY 4 KTVNGTAYDVVDVVDKSHENPMGTILFGGTGG-----APAPAAG 44  
 DB 5 KTVNGTAYDVVDVVDKSHENPMGTILFGGTGG-----EMGGAASAPAAPAPAPAPAPAPAPKPTT 57  
 QY 45 GAGAGKAGEGEIPAPLAGTAVSKILVKEGDTKAGQTVLVLEAMKMETEINAPTDGKVEKV 104  
 DB 58 AAGAG-AGANTVTAPMPGTTILVGVCHAGDKVSKGDTLVLEAMKMEINAPHDGVVSEV 116  
 QY 105 LVKERDAVQGGQGLI 119  
 DB 117 RVQGGASVNVAGDILV 131

## RESULT 7

O9ZAA7 PRELIMINARY; PRT; 145 AA.  
 AC O9ZAA7;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Glutaconyl-CoA decarboxylase gamma subunit (EC 4.1.1.70).  
 GN GCDC.  
 OS Acidaminococcus fermentans.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Acidaminococcaceae;  
 OC Acidaminococcus.  
 CX NCBI\_TaxID=905;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 25085;  
 RX MEDLINE=99157555; PubMed=10027965;  
 RA Braune A., Bendrat K., Rospert S., Buckel W.;  
 RT "The sodium ion translocating glutaconyl-CoA decarboxylase from  
 Acidaminococcus fermentans: cloning and function of the genes forming  
 a second operon";  
 RL Mol. Microbiol. 31:473-487(1999).  
 CC -I- COFACTOR: BIOTIN (BY SIMILARITY).  
 DR EMBL; AF030576; AAC69172.1; -;  
 DR HSSP; P02905; 1BD0.  
 DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0005840; C:ribosome; IEA.  
 DR GO; GO:0009374; F:biotin binding; IEA.  
 DR GO; GO:0018801; F:glutaconyl-CoA decarboxylase activity; IEA.  
 DR GO; GO:0016829; F:lyase activity; IEA.

[illegible]

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ID Q99ZL6 PRELIMINARY; PRT; 116 AA.
AC Q99ZL6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative methylmalonyl-CoA decarboxylase, gamma-subunit
DE (EC 4.1.1.41).
OS SPY1176.
GN Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=1192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Szate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -I- COFACTOR: BIOTIN (BY SIMILARITY).
DR EMBL; AE006558; AAK34043.1; -.
DR HSP; P02905; IED0.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0004492; F:methylmalonyl-CoA decarboxylase activity; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; Biotin; 1.
KW Biotin; Lyase; Complete proteome.
SQ SEQUENCE 116 AA; 12288 MW; A245219AC595BFEC CRC64;

Query Match 30.6%; Score 188; DB 16; Length 116;
Best Local Similarity 41.5%; Pred. No. 4.9e-08;
Matches 51; Conservative 11; Mismatches 45; Indels 16; Gaps 3;

QY 2 KLKVTNGTAYDVVDV-----RELVDGEIVESQAPAPATKEMNANAGGGIQV 51
Db 3 RYEVTNGQVVEVSL-----RELVDGEIVESQAPAPATKEMNANAGGGIQV 51

QY 57 PAPIAGTVSKILVKEGTVKAGQTVLVLEAMKMETEINAPDGVKVKLVKRDVQGGQ 116
Db 52 KAPMSGTILSFATGKAVKGEAVLVLEAMKMETEINAPDGLVSKIHVVANQTVESQ 111

QY 117 GLI 119
Db 112 VLI 114

RESULT 11
Q9PP00 PRELIMINARY; PRT; 599 AA.
AC Q9PP00;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative pyruvate carboxylase B subunit (EC 6.4.1.1).
DR PYCB OR C00933C.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCITC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Kettle J.M., Churcher C.,
RA Baaham D., Chillingworth T., Davies R.M., Feltham T., Holroyd S.,
RA Jagers K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,

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RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
CC -I- COFACTOR: BIOTIN (BY SIMILARITY).
DR EMBL; AL139076; CAB73190.1; -.
DR PIR; D81367; D81367.
DR HSP; P20708; IGHC.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004736; F:pyruvate carboxylase activity; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000891; HMGL-like.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR PROSITE; PS00188; Biotin; 1.
KW Biotin; Complete proteome.
SQ SEQUENCE 599 AA; 65833 MW; E5C075E114E40444 CRC64;

Query Match 30.5%; Score 187.5; DB 16; Length 599;
Best Local Similarity 37.5%; Pred. No. 3.6e-07;
Matches 48; Conservative 15; Mismatches 40; Indels 25; Gaps 3;

QY 2 KLKVTNGTAYDVVDV-----DYDKSHENPMCTILFGGTTGGAPAPAGGAGAGK 50
Db 481 KFTVAVNGNKYHVEVSYPDKVNVKVRKEBK--NISSSTSSVDA----- 528

QY 51 AGGEETPAPLAGTVSKILVKEGTVKAGQTVLVLEAMKMETEINAPDGVKVKLVKRD 110
Db 529 --ENEVLGISGNVFKIYVNEGEVKSQAIWLEAMKMEIYNAPKDGIIILEICIKIGD 586

QY 111 AVQGGQGL 118
Db 587 TVNEGEVL 594

RESULT 12
Q8K7G1 PRELIMINARY; PRT; 116 AA.
AC Q8K7G1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative methylmalonyl-CoA decarboxylase gamma-subunit.
GN SPYM3_0824 OR SP51025.
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.;
RT "The genome of invasive Streptococcus pyogenes; a comparative analysis
RT of S. pyogenes SSI-1, SF370 and MGAS8232.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE014153; AAM79431.1; -.
DR EMBL; AP005144; BAC64120.1; -.

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DB 112 VLI 114

RESULT 14

Q8A737 PRELIMINARY; PRT; 144 AA.

ID Q8A737

AC Q8A737

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Biotin carboxyl carrier protein (BCCP).

GN BT1688.

OS Bacteroides thetaiotaomicron.

OC Bacteria: Bacteroidetes; Bacteroides (class); Bacteroidales;

OC Bacteroidaceae; Bacteroides.

NCBI\_TaxID=818;

RN [1]

RX SEQUENCE FROM N.A.

RC STRAIN=VPI-5482 / ATCC 29148;

RX MEDLINE=2250858; PubMed=12663928;

RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,

RA Chiang H.C., Hooper L.V., Gordon J.I.;

RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."

RL Science 299:2074-2076(2003).

DR ENBL; A2016932; AAO76795.1; -.

DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.

DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.

DR GO; GO:0009374; F:biotin binding; IEA.

DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.

DR InterPro; IPR001249; AccoA\_biotinCC.

DR InterPro; IPR001882; Biotin\_BS.

DR InterPro; IPR000089; Biotin\_lipoyl.

DR Pfam; PF00364; biotin\_lipoyl; 1.

DR PRINTS; PR01071; ACOABT0TINCC.

DR PROSITE; PS00188; BIOTIN; 1.

KW Complete proteome.

SQ SEQUENCE 144 AA; 15487 MW; 462383E2F85601E CRC64;

Query Match 30.1%; Score 185; DB 16; Length 144;

Best Local Similarity 39.0%; Pred. No. 1.1e-07;

Matches 46; Conservative 18; Mismatches 52; Indels 2; Gaps

QY 5 VTVNGTAYDVVDVD-KSHENPMGVTILFGGTGGAPAPAGAGAGAGAGAGEGIPAPLACT 63

DB 27 VEYNGTHYKVEKQKQKAPKPV-VVRPMNPSPAAPTTPVVKPAAPSTGKVGKSLPGV 85

QY 64 VSKILKQEGDTVKAGQTVLVLVLEAMKMETEINAPTDGKVKVLVKERDAVGGQGLIKI 121

DB 86 ILDIKYNVGDVKRGQTIIILEAMKMNINADKQKVTAINVVKGDSVLEGNDLVII 143

RESULT 15

Q9KUHI PRELIMINARY; PRT; 597 AA.

ID Q9KUHI

AC Q9KUHI

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Oxaloacetate decarboxylase, alpha subunit.

GN VC0550.

OS Vibrio cholerae.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

OC Vibrionaceae; Vibrio.

NCBI\_TaxID=666;

RN [1]

RX SEQUENCE FROM N.A.

RC STRAIN=El Tor N16961 / Serotype O1;

RX MEDLINE=20406833; PubMed=10952301;

RA Haideberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

RA Dodson R.J., Haft D.H., Hickley E.K., Peterson J.D., Umayam L.A.,

RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

RA McDonald L., Uitterback T., Fleischmann R.D., Nierman W.C., White O.,

RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
 RA Fraser C.M.; and  
 RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*  
 RT *cholerae*.";  
 RL Nature 406:477-483(2000).  
 CC -1- COFACTOR: BIOTIN (BY SIMILARITY).  
 DR EMBL: AE004141; AAF93718.1; --  
 DR PIR: G82308; G82308.  
 DR HSP; P02905; IBD0.  
 DR TIGR; VC0550; --  
 DR GO: GO:0009374; F:biotin binding; IEA.  
 DR GO: GO:0003824; F:catalytic activity; IEA.  
 DR GO: GO:0008948; F:oxaloacetate decarboxylase activity; IEA.  
 DR GO: GO:0006814; F:sodium ion transport; IEA.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR InterPro; IPR000891; HMGL-like.  
 DR InterPro; IPR005776; OadA.  
 DR InterPro; IPR003379; PYC OADA.  
 DR Pfam; PF00364; biotin\_lipoyl; 1.  
 DR Pfam; PF00682; HMGL-like; 1.  
 DR Pfam; PF02436; PYC OADA; 1.  
 DR TIGRFAMs; TIGR01108; oada; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 KW Biotin; Complete proteome.  
 SQ SEQUENCE 597 AA; 64795 MW; 033BF5F2209F5468 CRC64;

Query Match 30.1%; Score 185; DB 16; Length 597;  
 Best Local Similarity 39.3%; Pred. No. 5.7e-07;  
 Matches 46; Conservative 18; Mismatches 45; Indels 8; Gaps 2;

QY 5 VTVNGTAYDVDDVDKSHENPMGTILFGGGTGGAPAAAGAGAGAGAGGEGEIPAPLAGTV 64  
 DB 488 VKVDGVYDVEV-----GSGQLTSTVPAGQAAPKLAVATPQAEA-VAAPLAGTI 539

QY 65 SKLVKEGDITVKAQTVLVLEAMQMETEINAPTQKVKLVKRDVQGGQGLIKI 121  
 DB 540 FKIQVGQDEVAEGDVLIVLEAMQMETEIRAARSGVIELHVKEGDSVRVGCASLSL 596

RESULT 16

ID Q891Y8 PRELIMINARY; PRT; 986 AA.  
 AC Q891Y8;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Pyruvate carboxylase (EC 6.4.1.1).  
 GN CTC02224.  
 OS Clostridium tetani.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1513;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Massachusetts / E88;  
 RX MEDLINE=22457253; PubMed=12552129;  
 RA Brueggemann H., Baeumer S., Fricke W.F., Wietzer A., Liesegang H.,  
 RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,  
 RA Gottschalk G.;  
 RT "The genome sequence of *Clostridium tetani*, the causative agent of  
 RT tetanus disease.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).  
 DR EMBL: AE015943; AA036707.1; --  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0009374; F:biotin binding; IEA.  
 DR GO: GO:0016874; F:ligase activity; IEA.  
 DR GO: GO:0004736; F:pyruvate carboxylase activity; IEA.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR InterPro; IPR005482; Biotin\_carb.C.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR InterPro; IPR005479; Crase\_L.D2.  
 DR InterPro; IPR000891; HMGL-like.

DR InterPro; IPR003379; PYC OADA.  
 DR Pfam; PF02785; Biotin\_carb.C; 1.  
 DR Pfam; PF00364; Biotin\_lipoyl; 1.  
 DR Pfam; PF02786; CPSase\_L.D2; 1.  
 DR Pfam; PF00682; HMGL-like; 1.  
 DR Pfam; PF02436; PYC OADA; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 DR PROSITE; PS00867; CPSASE\_2; 1.  
 KW Ligase; Complete proteome.  
 SQ SEQUENCE 986 AA; 110669 MW; 8925F618B0A4B219 CRC64;

Query Match 30.1%; Score 185; DB 16; Length 986;  
 Best Local Similarity 51.3%; Pred. No. 1e-06;  
 Matches 39; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 46 AGAGKAGEGEIPAPLAGTVSKILVKGSDTVKAQTVLVLEAMQMETEINAPTQKVKVL 105  
 DB 909 AMADKEDKSQIGASIFGNISKILKEGTVNKGDRIVAEAMQMETNIVSTVTKVKKIF 968

QY 106 VKERDAVQGGQGLIKI 121  
 DB 969 VKENEQVKVQGLIKI 984

RESULT 17

ID Q58564 PRELIMINARY; PRT; 571 AA.  
 AC Q58564;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE 571AA long hypothetical oxaloacetate decarboxylase alpha chain.  
 GN PH0834.  
 OS Pyrococcus horikoshii.  
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
 OC Pyrococcus.  
 OX NCBI\_TaxID=53953;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=OT3;  
 RX MEDLINE=98344137; PubMed=9679194;  
 RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,  
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,  
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,  
 RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kushida N., Oguchi A.,  
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb E.T., Horikoshi K.,  
 RA Masuchi Y., Shizuya H., Kikuchi H.;  
 RT "Complete sequence and gene organization of the genome of a hyper-  
 RT thermophilic archaeobacterium, *Pyrococcus horikoshii* OT3.";  
 RL DNA Res. 5:55-76(1998).  
 DR EMBL: AP000003; BAA29928.1; --  
 DR PIR: F71133; F71133.  
 DR HSP; P02905; IBD0.  
 DR GO: GO:0009374; F:biotin binding; IEA.  
 DR GO: GO:0003824; F:catalytic activity; IEA.  
 DR GO: GO:0008948; F:oxaloacetate decarboxylase activity; IEA.  
 DR GO: GO:0006814; F:sodium ion transport; IEA.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR InterPro; IPR000891; HMGL-like.  
 DR InterPro; IPR005776; OadA.  
 DR InterPro; IPR003379; PYC OADA.  
 DR Pfam; PF00364; biotin\_lipoyl; 1.  
 DR Pfam; PF00682; HMGL-like; 1.  
 DR Pfam; PF02436; PYC OADA; 1.  
 DR TIGRFAMs; TIGR01108; oada; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 571 AA; 64748 MW; B308B0B1C0E5B103 CRC64;

Query Match 29.9%; Score 184; DB 17; Length 571;  
 Best Local Similarity 37.5%; Pred. No. 6.5e-07;  
 Matches 45; Conservative 24; Mismatches 43; Indels 8; Gaps 3;

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QY 3 LKVTNGTAYDVVD-VDKSHENPMGTILFGGTTGAPAPAGAGAGAGAGGEGEIPAPILA 61
Db 458 IKIYINGKEFEVFEIGIEPEPKPKQDV---QAIQSPPKREVAPSGSV-----VSAPWP 510

QY 62 GTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVGGQGLIKI 121
Db 511 GKVLRLVRVGRVVRVGGQLLVLEAMKMETEINAPTDGKVEKVLVKERDAVGGQGLIEL 570

RESULT 18
ID Q8R7M0 PRELIMINARY; PRT; 122 AA.
AC Q8R7M0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Biotin carboxyl carrier protein.
GN ACCB2 OR TTE2383.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae;
OX NCBI_TaxID=119072;

SEQUENCE FROM N.A.
RP STRAIN=MB4 / JCM 11007;
RC MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR GO: 0009374; AAM25522.1; -.
DR EMBL: AB013180; AAM25522.1; -.
DR GO: 0009374; F:biotin binding; IEA.
DR InterPro: IPR001882; Biotin_BS.
DR InterPro: IPR000089; Biotin_lipoyl.
DR Pfam: PF00364; Biotin_lipoyl; 1.
DR PROSITE: PS00188; BIOTIN; 1.
KW Complete proteome.
SQ SEQUENCE 122 AA; 13437 MW; 649BFC4629C337C5 CRC64;

Query Match 29.2%; Score 179.5; DB 16; Length 122;
Best Local Similarity 34.5%; Pred. No. 2.6e-07;
Matches 48; Conservative 12; Mismatches 36; Indels 43; Gaps 3;

QY 2 LKVTNGTAYDVVDV-----DVKSHENPMGTILFGGTTGAPGA 40
Db 3 KFKVTNGKTYEVEEMKAEKEKSKKEIVEVEVPKQEK----- 46

QY 41 PAAGGAGAGAGGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGK 100
Db 47 -----VSTGK-GSKVVSAPMPGTTILDVRVKEGDRVKRGDVLVILEAMKMETEINAPDGI 100

QY 101 VEKVLVKERDAVGGQGLI 119
Db 101 VASVNVSKGASVNTGDLV 119

RESULT 19
Q8U917 PRELIMINARY; PRT; 576 AA.
AC Q8U917;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Biotin carboxylase.
GN ATU3913 OR AGR_L 1864.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN 11
RP SEQUENCE FROM N.A.

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RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutyavan T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
CS8.";
RL Science 294:2317-2323(2001).

RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L.,
RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Iartchouk O., Epp A., Liu F.,
RA Hummel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollman C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328(2001).
DR EMBL: AE009322; AAL44721.1; -.
DR EMBL: AE008292; AAK89506.1; -.
DR PIR: AC3038; AC3038.
DR PIR: H98247; H98247.
DR GO: 0005524; F:ATP binding; IEA.
DR GO: 0009374; F:biotin binding; IEA.
DR GO: 0016874; F:ligase activity; IEA.
DR GO: 0008152; P:metabolism; IEA.
DR InterPro: IPR001882; Biotin_BS.
DR InterPro: IPR005482; Biotin_carb_C.
DR InterPro: IPR000089; Biotin_lipoyl.
DR InterPro: IPR005479; CPase_L_D2.
DR InterPro: IPR005481; CPase_L_N.
DR Pfam: PF02785; Biotin_carb_C; 1.
DR Pfam: PF00364; Biotin_lipoyl; 1.
DR Pfam: PF00289; CPase_L_Chain; 1.
DR Pfam: PF02786; CPase_L_D2; 1.
DR PROSITE: PS00188; BIOTIN; 1.
DR PROSITE: PS00867; CPASE_2; 1.
KW Complete proteome.
SQ SEQUENCE 576 AA; 61722 MW; E0299479A952581F CRC64;

Query Match 28.7%; Score 176.5; DB 16; Length 576;
Best Local Similarity 43.8%; Pred. No. 2.7e-06;
Matches 42; Conservative 17; Mismatches 28; Indels 9; Gaps 3;

QY 26 MTILFGGTTGAPAPAGAGAGAGAGGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLE 85
Db 488 LGTV--SGNASAPSAV-----EKKEGEMTAPVSGTILQSFVKDGEIVSEGDLLAVNE 539

QY 86 AMKMETEINAPTDGKVEKVLVKERDAVGGQGLIKI 121
Db 540 AMKMETQIVATRAKGV-RLIVKEGDTVLAQATLIDI 574

RESULT 20
Q9WZH6 PRELIMINARY; PRT; 134 AA.
ID Q9WZH6
AC Q9WZH6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Propionyl-CoA carboxylase, gamma subunit.
GN TM0717.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;

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RN  SEQUENCE FROM N.A.
RP  STRAIN=MSB8 / DSM 3109;
RC  MEDLINE=99287316; PubMed=10360571;
RX  Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA  Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA  McDonald L., Uterback T.R., Matek J.A., Linher K.D., Garrett M.M.,
RA  Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA  Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA  Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT  "Evidence for lateral gene transfer between Archaea and Bacteria from
RT  genome sequence of Thermotoga maritima.";
RL  Nature 399:323-329(1999).
DR  EMBL: AE001743; AAD35799.1; -.
DR  PIR: C72341; C72343.
DR  HSP: P02905; IBD0.
DR  TIGR: TM0717; -.
DR  InterPro: IPR000089; Biotin_lipoyl.
DR  Pfam: PF00364; biotin_lipoyl; 1.
KW  Complete proteome.
SQ  SEQUENCE 134 AA; 15131 MW; A3BFBAAACE8574EC1 CRC64;

Query Match      28.6%; Score 176; DB 16; Length 134;
Best Local Similarity 33.6%; Pred. No. 5.5e-07;
Matches 49; Conservative 18; Mismatches 37; Indels 42; Gaps 4;

QY  2 KLVTVNGTAYDVVDV-----VDKSH-----ENPMGTILFGGTTGA 38
Db  4 KFRVVGNGKYYVEVEIGNVRKKEPAKEVSKTQVEIPEKPEKPVVL----- 55
QY  39 PAPAAGGAGAGKAGEGE---IPAPLAGTGVSKILVKEGDTVKAGQTVLVLEAMKMETEINAP 95
Db  56 -----EREKSSDQEKLVKAPMAGIVLVKLVKEGQKVNVDGLVLFVFEAMKMEINELQS 107
QY  96 PTKGVKEVLVKRDVAGQGGGLIKI 121
Db  108 EFGSTVKEILVKEGDNITGQILMKI 133

RESULT 21
Q48826 PRELIMINARY; PRT; 596 AA.
AC Q48826;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Oxaloacetate decarboxylase alpha-chain.
GN OADA.
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=446;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Corby;
RX MEDLINE=97120897; PubMed=8961567;
RA Jain B., Brand B.C., Lueck P.C., Di Bevardino M., Dimroth P.,
RA Hacker J.;
RT "An oxaloacetate decarboxylase homologue protein influences the
RT intracellular survival of Legionella pneumophila.";
RL FEMS Microbiol. Lett. 145:273-279(1996).
CC -|- COFACTOR: BIOTIN (BY SIMILARITY).
DR EMBL: X99678; CAA67994.1; -.
DR HSP: P11961; LLAB.
DR GO: GO:0009374; F:biotin binding; IEA.
DR GO: GO:0003824; F:catalytic activity; IEA.
DR GO: GO:0008948; F:oxaloacetate decarboxylase activity; IEA.
DR GO: GO:0006520; P:amino acid metabolism; IEA.
DR GO: GO:0006814; P:sodium ion transport; IEA.
DR InterPro: IPR001882; Biotin_BS.
DR InterPro: IPR000089; Biotin_lipoyl.
DR InterPro: IPR000891; HMGL-like.
DR InterPro: IPR005776; Oada.

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DR InterPro: IPR003379; PYC OADA.
DR InterPro: IPR000634; S/T_dehydrtse_BS.
DR Pfam: PF00364; biotin_lipoyl; 1.
DR Pfam: PF00682; HMGL-like; 1.
DR Pfam: PF02436; PYC OADA; 1.
DR TIGRFAMS: TIGR01108; Oada; 1.
DR TIGRFAMS: PS00188; BIOTIN; 1.
DR PROSITE: PS00165; DEHYDRATASE_SER_THR; 1.
KW Biotin.
SQ SEQUENCE 596 AA; 65667 MW; 55DBEAF96919C86 CRC64;

Query Match      28.6%; Score 176; DB 2; Length 596;
Best Local Similarity 51.4%; Pred. No. 3.1e-06;
Matches 37; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

QY  50 KAGEGIPAPLAGTGVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVLVKR 109
Db  522 KTGPGDITVAIFGSIITAIHVSAGDEVKAGQAVLVIEAMKMETEIKAPANGVVAEILCQKG 581
QY  110 DAVOGGGGLIKI 121
Db  582 DKVTFQGVLRV 593

RESULT 22
Q9XBJ1 PRELIMINARY; PRT; 984 AA.
AC Q9XBJ1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pyruvate carboxylase (EC 6.4.1.1) (Fragment).
GN PYCA.
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10987;
RX MEDLINE=99231848; PubMed=10217496;
RA Okstad O.A., Hegna I., Lindbaeck T., Rishovd A.L., Kolsto A.B.;
RA "Genome organisation is not conserved between Bacillus cereus and
RA Bacillus subtilis.";
RL Microbiology 145:621-631(1999).
DR EMBL: AJ010111; CAB40604.1; -.
DR PIR: T44608; T44608.
DR HSP: P24182; IDV2.
DR GO: GO:0005737; C:cytoplasm; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0016874; F:ligase activity; IEA.
DR GO: GO:0004736; F:pyruvate carboxylase activity; IEA.
DR GO: GO:0006094; P:gluconeogenesis; IEA.
DR InterPro: IPR005482; Biotin_carb_C.
DR InterPro: IPR000089; Biotin_lipoyl.
DR InterPro: IPR005479; Cphase_L_D2.
DR InterPro: IPR000891; HMGL-like.
DR InterPro: IPR003379; PYC OADA.
DR InterPro: IPR005930; Pyruv_carbox.
DR Pfam: PF02785; Biotin_carb_C; 1.
DR Pfam: PF00364; biotin_lipoyl; 1.
DR Pfam: PF02786; CPhase_L_D2; 1.
DR Pfam: PF00682; HMGL-like; 1.
DR Pfam: PF02436; PYC OADA; 1.
DR TIGRFAMS: TIGR01235; pyruv_carbox; 1.
DR PROSITE: PS00867; CPSASE_2; 1.
KW Ligase.
SQ SEQUENCE 984 AA; 110135 MW; 7AB52F8D453A147D CRC64;

Query Match      28.6%; Score 176; DB 2; Length 984;
Best Local Similarity 33.8%; Pred. No. 5.5e-06;
Matches 45; Conservative 19; Mismatches 49; Indels 20; Gaps 2;

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QY 9 GTAYDVVDVVDK-----HENPMGTILFGGGTGGAP-----APAAGGAGA 48
Db 850 GEEIDVEIQGKTLMLVKLVISIGEPQDGNRVLYLEFNGQPREIVVKDESVAQVRVGK 909
QY 49 GKAGEGEIPAPLAGTGVSKLVKEGDVTAKAGQTVLVLEAMKMETEINAPTDGKVKVVLKKE 108
Db 910 NRENPNHISATMGTVGVKVVKEGDEVKKGDSMAITEAMKMETTVOAPFNGKVKVYVND 969

QY 109 RDAVQGGGLIKI 121
Db 970 GDAIQTGDLIEL 982

RESULT 23
Q819M9 PRELIMINARY; PRT; 1148 AA.
AC Q819M9;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Pyruvate carboxylase (EC 6.4.1.1).
GN BC3947.
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatal V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AB017010; AAP10867.1; -
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004736; F:pyruvate carboxylase activity; IEA.
DR GO; GO:0006094; P:gluconeogenesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005482; Biotin carb. C.
DR InterPro; IPR000089; Biotin lipoyl.
DR InterPro; IPR005479; C:ase L D2.
DR InterPro; IPR005481; C:ase L N.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC OADA.
DR InterPro; IPR005930; Pyruv. carbox.
DR Pfam; PF02785; Biotin carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPSase_L_D2; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC OADA; 1.
DR TIGRfam; TIGR01235; Pyruv. carbox; 1.
DR PROSITE; PS00866; CPSASE_1; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Ligase; Pyruvate; Complete proteome.
SQ SEQUENCE 1148 AA; 128442 MW; EE5CC5BA99D8E191 CRC64;

Query Match 28.6%; Score 176; DB 16; Length 1148;
Best Local Similarity 33.8%; Pred. No. 6.6e-06;
Matches 45; Conservative 19; Mismatches 49; Indels 20; Gaps 2;

QY 9 GTAYDVVDVVDK-----HENPMGTILFGGGTGGAP-----APAAGGAGA 48
Db 1014 GEEIDVEIQGKTLMLVKLVISIGEPQDGNRVLYLEFNGQPREIVVKDESVAQVRVGK 1073
QY 49 GKAGEGEIPAPLAGTGVSKLVKEGDVTAKAGQTVLVLEAMKMETEINAPTDGKVKVVLKKE 108
Db 1074 NRENPNHISATMGTVGVKVVKEGDEVKKGDSMAITEAMKMETTVOAPFNGKVKVYVND 1133

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QY 109 RDAVQGGGLIKI 121
Db 1134 GDAIQTGDLIEL 1146

RESULT 24
Q82YV7 PRELIMINARY; PRT; 133 AA.
AC Q82YV7;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sodium ion-translocating decarboxylase, biotin carboxyl carrier
DE protein.
GN EF3325.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927;
RA Paulsen I.T., Banerjee I., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
RA Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
RA Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
RA Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis.";
RL Science 299:2071-2074(2003).
DR EMBL; AE016957; AA082990.1; -
DR TIGR; EF3325; -
DR GO; GO:0009374; F:biotin binding; IEA.
DR InterPro; IPR001882; Biotin BS.
DR InterPro; IPR000089; Biotin lipoyl.
DR Pfam; PF00364; biotin lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Complete proteome.
SQ SEQUENCE 133 AA; 13655 MW; D828752A1C1ADEAF CRC64;

Query Match 28.5%; Score 175.5; DB 16; Length 133;
Best Local Similarity 37.2%; Pred. No. 6e-07;
Matches 48; Conservative 17; Mismatches 55; Indels 9; Gaps 2;

QY 2 KLVTVNGTAYDVVD-----VDKSHENPMGTILFGGGTGGAP-----PAAGGAGAGKAG 52
Db 4 KFKISIDGKEXLVENEIEGGVQPAPVAPQPTAPVATTETPAPAVEETPASAAQPAAPAG 63

QY 53 EGEIPAPLAGTGVSKLVKEGDVTAKAGQTVLVLEAMKMETEINAPTDGKVKVVLKRDVAV 112
Db 64 ADAMPAPMGTVLVKLVNVGDTVSENPQLLLEAMKMETEINAPTDGKVKVVLKRDVAV 123

QY 113 QGGGGLIKI 121
Db 124 NPGEPPLITI 132

RESULT 25
Q88C37 PRELIMINARY; PRT; 602 AA.
AC Q88C37;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Oxaloacetate decarboxylase, alpha subunit.
GN OADA OR P53346.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]

```



DR GO: GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR005482; Biotin carb C.  
 DR InterPro; IPR000089; Biotin lipoyl.  
 DR InterPro; IPR005479; CPase\_L\_D2.  
 DR InterPro; IPR005481; CPase\_L\_N.  
 DR InterPro; IPR000891; HMGL-like.  
 DR InterPro; IPR003379; PYC OADA.  
 DR InterPro; IPR005930; Pyruv carbox.  
 DR Pfam; PF02785; Biotin carb C; 1.  
 DR Pfam; PF00364; biotin lipoyl; 1.  
 DR Pfam; PF00289; CPase\_L\_chain; 1.  
 DR Pfam; PF02786; CPase\_L\_D2; 1.  
 DR Pfam; PF00682; HMGL-like; 1.  
 DR Pfam; PF02436; PYC OADA; 1.  
 DR TIGRfams; TIGR01235; pyruv carbox; 1.  
 DR PROSITE; PS00866; CPASE\_1; 1.  
 DR PROSITE; PS00867; CPASE\_2; 1.  
 DR Pyruvate; Complete proteome.  
 SQ SEQUENCE 1148 AA; 128573 MW; 57B97F8D9D1287BF CRC64;  
 Query Match 28.5%; Score 175; DB 16; Length 1148;  
 Best Local Similarity 45.1%; Pred. No. 7.9e-06;  
 Matches 37; Conservative 14; Mismatches 31; Indels 0; Gaps 0;  
 QY 40 APAAGAGAGKAGEGEIPAPLACTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTGD 99  
 Db 1065 ATVAQVKVGNRENPNHISATMPGTIVKVVVKEGDEVKKGDSMAITKMETITVQAPPNG 1124  
 QY 100 KVEKVLVKERDAVQGGQGLIKI 121  
 Db 1125 KVKVYVNDGDAIQTDLLIEL 1146  
 RESULT 28  
 Q8RFP0 PRELIMINARY; PRT; 456 AA.  
 ID Q8RFP0  
 AC Q8RFP0  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Acyl-CoA carboxylase.  
 GN ACCBC OR CE0719.  
 OS Corynebacterium efficiens.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
 OX NCBI\_TaxID=152794;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;  
 RA Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,  
 RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,  
 RA Usuda Y., Sugimoto S.;  
 RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR GO: GO:0005216; BAC17529.1; -  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0009374; F:biotin binding; IEA.  
 DR GO: GO:0016874; F:ligase activity; IEA.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR InterPro; IPR005482; Biotin carb C.  
 DR InterPro; IPR000089; Biotin lipoyl.  
 DR Pfam; PF02785; Biotin carb C; 1.  
 DR Pfam; PF00364; biotin lipoyl; 1.  
 DR Pfam; PF02786; CPase\_L\_D2; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 DR PROSITE; PS00867; CPASE\_2; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 456 AA; 48958 MW; 748919EAC7679EE0 CRC64;  
 Query Match 28.3%; Score 174; DB 16; Length 456;  
 Best Local Similarity 36.3%; Pred. No. 3.3e-06;  
 Matches 45; Conservative 20; Mismatches 45; Indels 14; Gaps 3;  
 QY 2 KLKVTVNGTAYDVVDVVDKSHENPNMGTILFGGGTGGAP-----AAGGAGAGKAGEGEIP 57  
 Db 342 KVIIVEIDGRRVEALP-----GDLALGGGAGAAKKPKKRRAGGAKAGVSGD-SVA 391  
 QY 58 APLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTGDVKVKLVKERDAVQGGOG 117  
 Db 392 APMQGTIVKVNVEDGAEVSEGDVTVVLEAMKMNFPVKAHKSQTVSGLTIAAGEGVTKGV 451  
 QY 118 LIKI 121  
 Db 452 LLEI 455  
 RESULT 29  
 Q8RQNA PRELIMINARY; PRT; 591 AA.  
 ID Q8RQNA  
 AC Q8RQNA  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Acyl-CoA carboxylase B and C subunit.  
 GN ACCBC.  
 OS Corynebacterium efficiens.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
 OX NCBI\_TaxID=152794;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hirano S., Kimura E., Kawahara Y., Sugimoto S.;  
 RT "accBC of Corynebacterium efficiens.";  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 CC -I- COPACTOR: BIOTIN (BY SIMILARITY).  
 DR EMBL; AB083052; BAB89668.1; -  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0009374; F:biotin binding; IEA.  
 DR GO: GO:0016874; F:ligase activity; IEA.  
 DR GO: GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR InterPro; IPR005482; Biotin carb C.  
 DR InterPro; IPR000089; Biotin lipoyl.  
 DR InterPro; IPR005479; CPase\_L\_D2.  
 DR InterPro; IPR005481; CPase\_L\_N.  
 DR Pfam; PF02785; Biotin carb C; 1.  
 DR Pfam; PF00364; biotin lipoyl; 1.  
 DR Pfam; PF00289; CPase\_L\_chain; 1.  
 DR Pfam; PF02786; CPase\_L\_D2; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 DR PROSITE; PS00867; CPASE\_2; 1.  
 KW Biotin.  
 SQ SEQUENCE 591 AA; 63256 MW; 345BCEC36C5D8ACA CRC64;  
 Query Match 28.3%; Score 174; DB 2; Length 591;  
 Best Local Similarity 36.3%; Pred. No. 4.4e-06;  
 Matches 45; Conservative 20; Mismatches 45; Indels 14; Gaps 3;  
 QY 2 KLKVTVNGTAYDVVDVVDKSHENPNMGTILFGGGTGGAP-----AAGGAGAGKAGEGEIP 57  
 Db 477 KVIIVEIDGRRVEALP-----GDLALGGGAGAAKKPKKRRAGGAKAGVSGD-SVA 526  
 QY 58 APLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTGDVKVKLVKERDAVQGGOG 117  
 Db 527 APMQGTIVKVNVEDGAEVSEGDVTVVLEAMKMNFPVKAHKSQTVSGLTIAAGEGVTKGV 586  
 QY 118 LIKI 121  
 Db 587 LLEI 590  
 RESULT 30  
 Q8K7F5 PRELIMINARY; PRT; 131 AA.  
 ID Q8K7F5  
 AC Q8K7F5

DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Putative decarboxylase gamma chain.  
 GN SPIM3\_0830.  
 OS Streptococcus pyogenes (serotype M3).  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=198466;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MGAS315 / Serotype M3;  
 RX MEDLINE=22133808; PubMed=12122206;  
 RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,  
 RA Mammatella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,  
 RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,  
 RA Schlievert P.M., Mueser J.M.;  
 RT "Genome sequence of a serotype M3 strain of group A Streptococcus:  
 RT phage-encoded toxins, the high-virulence phenotype, and clone  
 RT emergence.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).  
 DR EMBL; AE014153; AAM79437.1; -  
 DR GO; GO:0009374; F:biotin binding; IEA.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR Pfam; PF00364; biotin\_lipoyl.1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 DR Complete proteome; Hypothetical protein.  
 KW SEQUENCE 131 AA; 13397 MW; 2FFD98C2487FB29E CRC64;  
 SQ SEQUENCE 131 AA; 13397 MW; 2FFD98C2487FB29E CRC64;  
 Query Match 28.2%; Score 173.5; DB 16; Length 131;  
 Best Local Similarity 32.4%; Pred. No. 8.5e-07;  
 Matches 47; Conservative 15; Mismatches 42; Indels 41; Gaps 2;  
 Qy 2 KLKVTNGTAYDVVDVVDKSHENPMGTILFGGGTGGAPAPAAGCA----- 46  
 Db 4 KFKTIDGKEYLVE-----EIGAPAQAAPAAQPISTPVPVTEASP 46  
 Qy 47 -----GAGKAGEGEIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPT 97  
 Db 47 QVEEAQAPQVAAAGADAIPSPMGITLKVLVAVGQVTENQPLILLEAMKMEINEIVASS 106  
 Qy 98 DGKVEKLVKRDVAVGGGGLIKIG 122  
 Db 107 AGTITAHVGPQGVNPGDGLITIG 131  
 RESULT 31  
 Q99ZL1 PRELIMINARY; PRT; 132 AA.  
 AC Q99ZL1  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Putative decarboxylase, gamma chain.  
 GN SPY1183.  
 OS Streptococcus pyogenes.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1314;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SF370 / ATCC 700294 / Serotype M1;  
 RX MEDLINE=21192684; PubMed=11296296;  
 RA Perretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,  
 RA Primeaux C., Szatze S., Suworov A.N., Kenton S., Lai H.S., Lin S.P.,  
 RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,  
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;  
 RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).  
 CC -1- COPACTOR: BIOTIN (BY SIMILARITY).  
 DR EMBL; AE006559; AAK34049.1; -  
 DR HSSP; P02905; 3BDO.

DR GO; GO:0009374; F:biotin binding; IEA.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR Pfam; PF00364; biotin\_lipoyl.1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 DR Biotin; Complete proteome.  
 KW SEQUENCE 132 AA; 13529 MW; 2FA2B1FB8119429E CRC64;  
 SQ SEQUENCE 132 AA; 13529 MW; 2FA2B1FB8119429E CRC64;  
 Query Match 28.2%; Score 173.5; DB 16; Length 132;  
 Best Local Similarity 32.4%; Pred. No. 8.6e-07;  
 Matches 47; Conservative 15; Mismatches 42; Indels 41; Gaps 2;  
 Qy 2 KLKVTNGTAYDVVDVVDKSHENPMGTILFGGGTGGAPAPAAGCA----- 46  
 Db 5 KFKTIDGKEYLVE-----EIGAPAQAAPAAQPISTPVPVTEASP 47  
 Qy 47 -----GAGKAGEGEIPAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPT 97  
 Db 48 QVEEAQAPQVAAAGADAIPSPMGITLKVLVAVGQVTENQPLILLEAMKMEINEIVASS 107  
 Qy 98 DGKVEKLVKRDVAVGGGGLIKIG 122  
 Db 108 AGTITAHVGPQGVNPGDGLITIG 132  
 RESULT 32  
 Q97VY7 PRELIMINARY; PRT; 186 AA.  
 AC Q97VY7  
 DT 01-OCT-2001 (TREMBlrel. 18, Created)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Biotin carboxyl carrier protein of propionyl-CoA carboxylase beta  
 DE subunit (EC 6.4.1.3).  
 GN SSO2484.  
 OS Sulfolobus solfataricus.  
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
 OC Sulfolobus.  
 OX NCBI\_TaxID=2287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;  
 RX MEDLINE=21332296; PubMed=11427726;  
 RA She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,  
 RA Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,  
 RA De Moers A., Brauso G., Fletcher C., Gordon P.M.K.,  
 RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,  
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,  
 RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,  
 RA Garrett R.A., Ragan M.A., Senses C.W., Van der Oost J.;  
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840 (2001).  
 DR EMBL; AE006845; AAK42603.1; -  
 DR PIR; D90418; D90418.  
 DR GO; GO:0009374; F:biotin binding; IEA.  
 DR GO; GO:0016874; F:ligase activity; IEA.  
 DR GO; GO:0004658; F:propionyl-CoA carboxylase activity; IEA.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR Pfam; PF00364; biotin\_lipoyl.1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 DR Ligase; Complete proteome.  
 KW SEQUENCE 186 AA; 21166 MW; DB26587C39883B08 CRC64;  
 Query Match 28.2%; Score 173.5; DB 17; Length 186;  
 Best Local Similarity 40.0%; Pred. No. 1.3e-06;  
 Matches 50; Conservative 14; Mismatches 42; Indels 19; Gaps 4;  
 Qy 7 VNGTAYDVVDVVDKSHENPMGTILFGGG-----TGGAPAPAAGGAGA-----GKAGEGEI 56  
 Db 70 INGKXYVFIED-----GTLFPHQDFLRDKVTEIPKGEERVEEIRGK--EGEI 120  
 Qy 57 PAPLAGTIVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTGDGKVKLVKRDVAVGGG 116



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121 VSPLEGRVVKLRVKEGDVAVKNGQPLLSIEMKAETVISSPGIGVQKILIKEGQGVKGD 180
QY
117 GLIKI 121
181 ILIVI 185

RESULT 33
Q8XGX8
ID Q8XGX8 PRELIMINARY; PRT; 591 AA.
AC Q8XGX8;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE Oxaloacetate decarboxylase alpha chain (EC 4.1.1.3).
GN OADA OR STY3532 OR T0057 OR T3267.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodyanni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18."
RL J. Bacteriol. 185:2330-2337(2003).
DR EMBL; AL627278; CAD07867.1; -
DR EMBL; AL627265; CAD01210.1; -
DR EMBL; AB016834; AAC067790.1; -
DR EMBL; AB016845; AAC070802.1; -
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016929; F:lyase activity; IEA.
DR GO; GO:0008948; F:oxaloacetate decarboxylase activity; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001882; Biotin BS.
DR InterPro; IPR000089; Biotin lipoyl.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR005776; Oada.
DR Pfam; PF00364; biotin lipoyl; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PVC OADA; 1.
DR TIGRfams; TIGR01108; oada; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Lyase, Complete proteome.
SQ SEQUENCE 591 AA; 63372 MW; 10F3A3BE94AB7DD2 CRC64;

Query Match 28.2%; Score 173.5; DB 16; Length 591;
Best Local Similarity 40.2%; Pred. No. 4.9e-06;
Matches 47; Conservative 14; Mismatches 49; Indels 7; Gaps 3;

QY 5 VTVNGTAYDVVDVKSHENPMGTILFGGGTGGAPAGGAGKAGEIEIPAPLAGTV 64
Db 481 VEVEGKAFVVRVS-DGGDIISQLTTAV--PAASAPVQAAAPAGAGT----PVTAPLAGNI 533

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65 SKILVKEGDTVKAGQTVLLEAMKMETEINAPTDKGKVLVKERDAVQGGGLIKI 121
Db 534 WKVIATEGQSVAGEDVLLILEAMKMETEIRAAQAGTVRGIAVKSQSDAVSVGDTLMTL 590

RESULT 34
Q87U07
ID Q87U07 PRELIMINARY; PRT; 602 AA.
AC Q87U07;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Oxaloacetate decarboxylase, alpha subunit.
GN OADA OR PSPT05510.
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RA Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
RA Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,
RA Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
RA Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
RA White O., Fraser C., Collmer A.;
RT "Complete sequence of Pseudomonas syringae."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016876; AAC08929.1; -
DR TIGR; PSPT05510; -
DR GO; GO:0003824; P:catalytic activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR InterPro; IPR000089; Biotin lipoyl.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PVC OADA.
DR InterPro; IPR006344; S/T_Gendrtse_BS.
DR Pfam; PF00364; biotin lipoyl; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PVC OADA; 1.
DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
KW Complete proteome.
SQ SEQUENCE 602 AA; 65598 MW; BD644376294712E3 CRC64;

Query Match 28.0%; Score 172.5; DB 16; Length 602;
Best Local Similarity 33.1%; Pred. No. 6e-06;
Matches 45; Conservative 18; Mismatches 44; Indels 29; Gaps 3;

QY 5 VTVNGTAYDVVDV-----DVDSKHE-----NPMGTILFGGGTGGAPAPAGG 45
Db 475 IDVHGCTYRVDITGVGKAEGRKHFYLTIDGMPEEWFPEPLNEFVGGGASKSQQASA--- 531

QY 46 AGAGKAGEIEIPAPLAGTVSKILVKEGDTVKAGQTVLLEAMKMETEINAPTDKGKVL 105
Db 532 -----PGHVSTTWPFGNIVDLVKEGDDVVKAGQAVLITEAMKMETEQVASTAGKVVAIH 584

QY 106 VKERDAVQGGGLIKI 121
Db 585 VAKGDRVNPGEILVEI 600

RESULT 35
Q8R5Y8
ID Q8R5Y8 PRELIMINARY; PRT; 134 AA.
AC Q8R5Y8;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Biotin carboxyl carrier protein of glutamyl-CoA decarboxylase
DE (EC 4.1.1.70).
GN PN0200.
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteriales; Fusobacteriaceae;

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DR InterPro; IPR005482; Biotin carb C.  
DR InterPro; IPR000089; Biotin\_lipoYL.  
DR InterPro; IPR005479; CPhase\_L D2.  
DR InterPro; IPR005481; CPhase\_L N.  
DR InterPro; IPR000291; Dala\_lig Van.  
DR InterPro; IPR000891; HMGL-like.  
DR InterPro; IPR003379; PYC OADA.  
DR Pfam; PF02785; Biotin carb C; 1.  
DR Pfam; PF00364; biotin\_lipoYL; 1.  
DR Pfam; PF00289; CPhase\_L chain; 1.  
DR Pfam; PF02786; CPhase\_L D2; 1.  
DR Pfam; PF01820; Dala\_dala\_ligas; 1.  
DR Pfam; PF00682; HMGL-like; 1.  
DR Pfam; PF02436; PYC OADA; 1.  
DR PROSITE; PS00866; CPhase\_1; 1.  
DR PROSITE; PS00867; CPhase\_2; 1.  
DR KW Ligase; Complete proteome.  
DR SQ SSEQUENCE 1144 AA; 127299 MW; BFAFA8AD6325DCDF CRC64;

Query Match 27.9%; Score 171.5; DB 16; Length 1144;  
Best Local Similarity 34.5%; Pred. No. 1.5e-05;  
Matches 41; Conservative 20; Mismatches 41; Indels 17; Gaps 1;

QY 3 LKTVNGTAYDVVDVVDKSHENPMGILFGGTCGGAPAPAGGAGAGKAGEGTEIPAPLAG 62  
Db 1040 LYSFINGQNGQINMKVNAHQSATST-----RKAEPTNDEVGATMSG 1082

QY 63 TVSKILVKEGDTVKAGTQVLVLEAMKMETINAPTDCGKVKVLVKERDAVGGGGGLKI 121  
Db 1083 SVLKLLVKKGTQVKKEPFLVTEAMKMETTIQAPEDGVIEHYVYVAGDVICTDLDLLEI 1141

RESULT 37

Q87LNR PRELIMINARY; PRT; 595 AA.

ID Q87LNR AC Q87LNR; AC Q87LNR;  
DT 01-JUN-2003 (TEMBLrel. 24, Created)  
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)  
DE Oxaloacetate decarboxylase, alpha subunit.  
GN VP2544.  
OS Vibrio parahaemolyticus.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
OC Vibrionaceae; Vibrio.  
OX NCBI\_TaxID=670;  
RN [1]  
RZ SEQUENCE FROM N.A.  
RC STRAIN=RIMD 2210633 / Serotype O3:K6;  
RX MEDLINE=22508454; PubMed=12620739;  
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,  
RA Iijima Y., Najima M., Nakano M., Yanashita A., Kubota Y., Kimura S.,  
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;  
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism  
RT distinct from that of V. cholerae.";  
RL Lancet 361:743-749(2003).  
DR EMBL; AP005081; BAC60807.1; -  
DR GO; GO:009374; F:biotin binding; IEA.  
DR GO; GO:0003224; F:catalytic activity; IEA.  
DR InterPro; IPR001882; Biotin BS.  
DR InterPro; IPR000089; Biotin\_lipoYL.  
DR InterPro; IPR000891; HMGL-like.  
DR InterPro; IPR003379; PYC OADA.  
DR Pfam; PF00364; biotin\_lipoYL; 1.  
DR Pfam; PF00682; HMGL-like; 1.  
DR Pfam; PF02436; PYC OADA; 1.  
DR PROSITE; PS00188; BIOTIN; 1.  
DR KW Complete proteome.  
DR SQ SSEQUENCE 595 AA; 64275 MW; ODCE581EFBA22FOA CRC64;

Query Match 27.8%; Score 171; DB 16; Length 595;  
Best Local Similarity 37.6%; Pred. No. 7.9e-06;  
Matches 44; Conservative 15; Mismatches 50; Indels 8; Gaps 2





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 3, 2004, 10:24:54 ; Search time 7.29167 Seconds  
(without alignments)  
499.873 Million cell updates/sec

Title: US-09-987-485A-2

Perfect score: 342

Sequence: 1 EGISAPLACTVSKILVKEG.....KVLVKERDVGQGLIKIG 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	342	100.0	123	1	BCCP_PROPR
2	173	50.6	567	1	PYCB_MERJA
3	165	48.2	595	1	DCOA_KLEPN
4	152	44.4	590	1	DCOA_SALTY
5	148	43.3	717	1	MCCA_MOUSE
6	145	42.4	130	1	BCCP_STRMU
7	143	41.8	70	1	BCCP_LYCES
8	143	41.8	725	1	MCCA_HUMAN
9	143	41.8	734	1	MCCA_ARATH
10	140	40.9	568	1	PYCB_MERTH
11	138.5	40.5	157	1	BCCP_PORPU
12	138	40.4	1180	1	PYC2_YEAST
13	133	38.9	1178	1	PYCI_YEAST
14	132	38.6	1189	1	PYC1_FICPA
15	130	38.0	598	1	BCCA_MYCLE
16	130	38.0	731	1	MCCA_SOYBN
17	129	37.7	1178	1	PYC_MOUSE
18	126.5	37.0	181	1	BCCP_ANASP
19	124.5	36.4	654	1	BCCA_MYCTU
20	122	35.7	164	1	BCCP_CHLTR
21	121	35.4	1178	1	PYC_HUMAN
22	119	34.8	1178	1	PYC_RAT
23	118	34.5	70	1	BTB7_MYCSM
24	118	34.5	163	1	BCCP_CHLMU
25	115.5	33.8	547	1	ODP2_PSEAE
26	115	33.6	70	1	BTB7_MYCTU
27	114	33.3	438	1	ODP2_MYCCA
28	113.5	33.2	629	1	ODP2_ECOLI
29	111	32.5	704	1	PCCA_RAT
30	110	32.2	703	1	PCCA_HUMAN
31	108.5	31.7	167	1	BCCP_CHLPN
32	108	31.6	553	1	ODO2_MYCTU
33	107	31.3	70	1	BTB7_MYCLE

RESULT 1  
BCCP\_PROPR  
ID BCCP\_PROPR STANDARD; PRT; 123 AA.  
AC P02904;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Biotin carboxyl carrier protein of methylmalonyl-CoA carboxyl-  
transferase (Transcarboxylase, 1.3S subunit).  
OS Propionibacterium freudenreichii shermanii.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Propionibacterineae; Propionibacteriaceae; Propionibacterium.  
OX NCBI\_TaxID=1752;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85298212; PubMed=3898065;  
RA Murtif V.L., Bahler C.R., Samols D.;  
RT "Cloning and expression of the 1.3S biotin-containing subunit of  
transcarboxylase.";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:5617-5621(1985).  
RN [2]  
RP SEQUENCE.  
RX MEDLINE=80049796; PubMed=40985;  
RA Maloy W.L., Bowlen B.U., Zwolinski G.K., Kumar G.K., Wood H.G.,  
RA Ericsson L.H., Walsh K.A.;  
RT "Amino acid sequence of the biotinyl subunit from transcarboxylase.";  
RL J. Biol. Chem. 254:11615-11622(1979) ✓  
RN [3]  
RP MUTAGENESIS OF ALA-87; MET-88; LYS-89 AND MET-90.  
RX MEDLINE=92406744; PubMed=1526981;  
RA Shenoy B.C., Xie Y., Park V.L., Kumar G.K., Beegen H., Wood H.G.,  
RA Samols D.;  
RT "The importance of methionine residues for the catalysis of the  
biotin enzyme, transcarboxylase. Analysis by site-directed  
mutagenesis.";  
RL J. Biol. Chem. 267:18407-18412(1992).  
RN [4]  
RP STRUCTURE BY NMR.  
RX MEDLINE=98086416; PubMed=9398186;  
RA Reddy D.V., Shenoy B.C., Carey P.R., Soennichsen F.D.;  
RT "Absence of observable biotin-protein interactions in the 1.3S  
subunit of transcarboxylase: an NMR study.";  
RL Biochemistry 36:14676-14682(1997).  
CC -!- FUNCTION: THE BIOTINYL 1.3S SUBUNIT SERVES AS A CARBOXYL CARRIER  
BETWEEN THE SUBSTRATE BINDING SITES ON THE 12S AND 5S SUBUNITS.  
CC -!- SUBUNIT: TRANSCARBOXYLASE IS COMPOSED OF THREE SUBUNITS: 1.3S,  
5S, AND 12S. THE CORE OF THE ENZYME IS COMPOSED OF SIX 12S  
SUBUNITS. ON EACH SIDE OF THE CORE THERE ARE THREE PAIRS OF 5S  
SUBUNITS. EACH 5S DIMER IS ATTACHED TO THE CORE BY TWO 1.3S  
SUBUNITS. THE TOTAL NUMBER OF CHAINS IS 30 (6 + 12 + 12).  
CC -----  
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34 104 30.4 1835 1 DURL\_YEAST  
35 103.5 30.3 567 1 ODP2\_HAEIN  
36 103 30.1 462 1 ODPB\_ZYMMO  
37 102.5 30.0 155 1 BCCP\_HAEIN  
38 102 29.8 544 1 ODP2\_ACHLA  
39 102 29.8 637 1 ODP2\_AZOVI  
40 101.5 29.7 262 1 BCCP\_SOYBN  
41 98.5 28.8 156 1 BCCP\_PSEAE  
42 97.5 28.5 156 1 BCCP\_ECOLI  
43 97 28.4 384 1 ODP2\_MYCGE  
44 95 27.8 463 1 ODO2\_YEAST  
45 94.5 27.6 152 1 BCCP\_CYACA

#### ALIGNMENTS

P32528 saccharomyc  
P45118 haemophilus  
O66113 zymomonas m  
P43874 haemophilus  
P35489 acholeplasm  
P10802 azotobacter  
Q42783 glycine max  
P37799 pseudomonas  
P02905 escherichia  
P47514 mycoplasma  
P19262 saccharomyc  
Q19918 cyanidium c

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 CC -----  
 DR EMBL; M11738; AAA25674.1; -.  
 DR PIR; A03401; BKIP.  
 DR PDB; 1DC2; 10-MAY-00.  
 DR PDB; 1DD2; 24-MAR-00.  
 DR PDB; 1O78; 21-NOV-02.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR Pfam; PF00364; biotin\_lipoyl; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 DR Biotin; 3D-structure.  
 FT BINDING 89  
 FT BINDING 89 BIOTIN  
 SQ SEQUENCE 123 AA; 12367 MW; D0980C2065EA9A89 CRC64;  
 Query Match 100.0%; Score 342; DB 1; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-26;  
 Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EGEIPAPLAGTTSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVKVLEKRDV 60  
 Db 54 EGEIPAPLAGTTSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVKVLEKRDV 113  
 QY 61 QGGQGLIKIG 70  
 Db 114 QGGQGLIKIG 123  
 RESULT 2  
 ID PYCB METJA STANDARD; PRT; 567 AA.  
 AC Q89628; 2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Pyruvate carboxylase subunit B (EC 6.4.1.1) (Pyruvic carboxylase B).  
 GN PYCB OR M1231.  
 OS Methanococcus jannaschii.  
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;  
 OC Methanocaldococcaceae; Methanocaldococcus.  
 OX NCBI\_TaxID=2190;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SFRAIN-JAL-1 / DSM 2661 / ATCC 43067;  
 RX MEDLINE=96337999; PubMed=868087;  
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,  
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,  
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,  
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,  
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,  
 RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
 RA Cotton M.D., Roberts K.M., Hurst W.A., Kaine B.P., Borodovsky M.,  
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;  
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus  
 jannaschii.";  
 RL Science 273:1058-1073 (1996).  
 RN [2]  
 RP SEQUENCE OF 190-125; 260-270; 277-289; 277-289; 309-325; 328-358;  
 RP 370-380; 386-409; 422-438; 491-506 AND 491-506, AND FUNCTION.  
 RX MEDLINE=21034791; PubMed=11195096;  
 RA Mukhopadhyay B., Patel V.J., Wolfe R.S.;  
 RT "A stable archaeal pyruvate carboxylase from the hyperthermophile  
 Methanococcus jannaschii.";  
 RL Arch. Microbiol. 174:406-414 (2000).  
 CC -!- FUNCTION: Pyruvate carboxylase catalyzes a 2-step reaction,  
 CC involving the ATP-dependent carboxylation of the covalently  
 CC attached biotin in the first step and the transfer of the carboxyl  
 CC group to pyruvate in the second.  
 CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +  
 CC oxaloacetate.  
 CC -!- COFACTOR: ATP, magnesium (or manganese or cobalt), pyruvate and  
 CC bicarbonate.

CC -!- ENZYME REGULATION: INHIBITED BY MAGNESIUM, WHEN ITS CONCENTRATION  
 CC EXCEEDED THE ATP ONE, AND BY HIGH CONCENTRATION OF ATP AND ALPHA-  
 CC KETOGLUTARATE.  
 CC -!- PATHWAY: Gluconeogenesis.  
 CC -!- SUBUNIT: Heterooctamer of four A and four B subunits.  
 CC -!- MASS SPECTROMETRY: MW=64160; METHOD=WALDI.  
 CC -!- MISCELLANEOUS: ITS OPTIMUM PH IS 8.5 AND THE OPTIMUM TEMPERATURE  
 CC IS 80-90 DEGREES CELSIUS.  
 CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES  
 CC AND CARBAMYL PHOSPHATE SYNTHETASES.  
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 CC -----  
 DR EMBL; U67563; AAB99233.1; -.  
 DR PIR; F64453; F64453.  
 DR HSP; P02905; 1A6X.  
 DR TIGR; M1231; -.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR InterPro; IPR000891; HMGL-like.  
 DR InterPro; IPR005776; Oada.  
 DR InterPro; IPR003379; PYC\_OADA.  
 DR Pfam; PF00364; biotin\_lipoyl; 1.  
 DR Pfam; PF00682; HMGL-like; 1.  
 DR Pfam; PF02436; PYC\_OADA; 1.  
 DR TIGRFAMs; TIGR01108; oada; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 KW Ligase; Multifunctional enzyme; Gluconeogenesis; Magnesium; Pyruvate;  
 KW Biotin; Complete proteome.  
 FT BINDING 52 60 PYRUVATE (BY SIMILARITY).  
 FT BINDING 53 533 BIOTIN (BY SIMILARITY).  
 SQ SEQUENCE 567 AA; 63907 MW; 5E07800622545628 CRC64;  
 Query Match 50.6%; Score 173; DB 1; Length 567;  
 Best Local Similarity 50.7%; Pred. No. 1.8e-09;  
 Matches 35; Conservative 12; Mismatches 22; Indels 0; Gaps 0;  
 QY 1 EGEIPAPLAGTTSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQKVKVLEKRDV 60  
 Db 498 EGAVTSPPFRGMVTKIKVKGDKYKGGDVIVLEAMKMEHPISPEVGTVERILDEGDAV 557  
 QY 61 QGGQGLIKI 69  
 Db 558 NVGDVIMII 566  
 RESULT 3  
 ID DCOA KLEPN STANDARD; PRT; 595 AA.  
 AC P13187;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE Oxaloacetate decarboxylase alpha chain (EC 4.1.1.3).  
 GN OADA.  
 OS Klebsiella pneumoniae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Klebsiella.  
 OX NCBI\_TaxID=573;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88257085; PubMed=2454915;  
 RA Schwarz E., Oesterheld D., Reinke H., Beyreuther K., Dimroth P.;  
 RT "The sodium ion translocating oxalacetate decarboxylase of Klebsiella  
 pneumoniae. Sequence of the biotin-containing alpha subunit and  
 RT relationship to other biotin-containing enzymes.";  
 RL J. Biol. Chem. 263:9640-9645 (1988).

CC -!- FUNCTION: Lyase and sodium transporter.  
 CC -!- CATALYTIC ACTIVITY: Oxaloacetate = pyruvate + CO(2).  
 CC -!- COFACTOR: Biotin and requires a sodium ion.  
 CC -!- SUBUNIT: Composed of three chains (alpha, beta, and gamma).  
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DR EMBL: J03885; AAA25120.1; -.  
 DR PIR: A28088; A28088.  
 DR HSRP: P02905; IAE6.  
 DR InterPro: IPR001882; Biotin BS.  
 DR InterPro: IPR000089; Biotin lipoyl.  
 DR InterPro: IPR000891; HMGL-like.  
 DR InterPro: IPR005776; Oada.  
 DR InterPro: IPR003379; PYC OADA.  
 DR Pfam: PF00364; Biotin\_lipoyl; 1.  
 DR Pfam: PF00682; HMGL-like; 1.  
 DR Pfam: PF02436; PYC OADA; 1.  
 DR TIGRFAMs: TIGR01108; oada; 1.  
 DR PROSITE: PS00188; BIOTIN; 1.  
 DR Decarboxylase; Lyase; Sodium transport; Biotin.  
 KW  
 FT INIT MET  
 FT BINDING 561 561 BIOTIN (BY SIMILARITY).  
 SQ SEQUENCE 595 AA; 63402 MW; AA744A95A6E9488C CRC64;

Query Match 48.2%; Score 165; DB 1; Length 595;  
 Best Local Similarity 53.0%; Pred No. 1,1e-08;  
 Matches 35; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

QY 4 IPAPLAGTIVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKLVKRDVAVGG 63  
 DB 529 VTAPLAGTIVKVLASEGQTVAAEGLVLLLEAMKMETEIRAAQAGTVRGIAKAGDAVAVG 588

QY 64 QGLIKI 69

DB 589 DTLMTL 594

## RESULT 4

ID DCOA\_SALTY STANDARD; PRT; 590 AA.  
 AC Q03030;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Oxaloacetate decarboxylase alpha chain (EC 4.1.1.3).  
 GN (OADA1 OR OADA OR STM0055) AND (OADA2 OR STM3352).  
 OS Salmonella typhimurium.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 OX NCBI\_TaxID=602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LT2;  
 RX MEDLINE=93054591; PubMed=1331067;  
 RA Woelke G., Wifling K., Dimroth P.,  
 RT "Sequence of the sodium ion pump oxaloacetate decarboxylase from  
 RT Salmonella typhimurium";  
 RL J. Biol. Chem. 267:22798-22803 (1992).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;  
 RX MEDLINE=21534948; PubMed=11677609;  
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Forwellik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
 RN [2]

RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium  
 RT LT2.";  
 RL Nature 413:852-856(2001).  
 CC -!- FUNCTION: Lyase and sodium transporter.  
 CC -!- CATALYTIC ACTIVITY: Oxaloacetate = pyruvate + CO(2).  
 CC -!- COFACTOR: Biotin and requires a sodium ion.  
 CC -!- SUBUNIT: Composed of three chains (alpha, beta, and gamma).  
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DR EMBL: M96434; AAA02973.1; -.  
 DR EMBL: AE008696; AAL19019.1; -.  
 DR EMBL: AE008854; AAL22221.1; -.  
 DR PIR: B44465; B44465.  
 DR HSRP: P02905; IAE6.  
 DR StyGene; SG10259; oada1.  
 DR StyGene; SG7777; oada2.  
 DR InterPro: IPR001882; Biotin BS.  
 DR InterPro: IPR000089; Biotin lipoyl.  
 DR InterPro: IPR000891; HMGL-like.  
 DR InterPro: IPR005776; Oada.  
 DR InterPro: IPR003379; PYC OADA.  
 DR Pfam: PF00364; Biotin\_lipoyl; 1.  
 DR Pfam: PF00682; HMGL-like; 1.  
 DR Pfam: PF02436; PYC OADA; 1.  
 DR TIGRFAMs: TIGR01108; oada; 1.  
 DR PROSITE: PS00188; BIOTIN; 1.  
 DR Decarboxylase; Lyase; Sodium transport; Biotin; Complete proteome.  
 KW  
 FT INIT MET  
 FT BINDING 556 556 BIOTIN (BY SIMILARITY).  
 SQ SEQUENCE 590 AA; 63075 MW; 4EA421F9324AFD7B CRC64;

Query Match 44.4%; Score 152; DB 1; Length 590;

Best Local Similarity 48.5%; Pred No. 2e-07;  
 Matches 32; Conservative 9; Mismatches 25; Indels 0; Gaps 0;

QY 4 IPAPLAGTIVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKLVKRDVAVGG 63  
 DB 524 VTAPLAGTIVKVLASEGQTVAAEGLVLLLEAMKMETEIRAAQAGTVRGIAKAGDAVAVG 583

QY 64 QGLIKI 69

DB 584 DTLMTL 589

## RESULT 5

ID MCCA\_MOUSE STANDARD; PRT; 717 AA.  
 AC Q99MR8; Q99MR8;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor  
 DE (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha  
 DE subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase alpha subunit).  
 GN MCC1 OR MCCA.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RX MEDLINE=21102410; PubMed=11181649;  
 RA Baumgartner M.R., Almashanu S., Suormala T., Obie C., Cole R.N.,  
 RA Packman S., Baumgartner E.R., Valle D.;

RT "The molecular basis of human 3-methylcrotonyl-CoA carboxylase  
 RT deficiency.";  
 RL J. Clin. Invest. 107:495-504 (2001).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690 (2001).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Kidney;  
 RC MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Heide F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield A.S., Schein J.E., Jones S.J.M., Marra M.A.,  
 RA Schnerch A., Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 CC -1- CATALYTIC ACTIVITY: ATP + 3-methylcrotonyl-CoA + HCO(3) (-) = ADP +  
 CC phosphate + 3-methylglutaconyl-CoA.  
 CC -1- COFACTOR: Biotin.  
 CC -1- PATHWAY: Leucine catabolism.  
 CC -1- SUBUNIT: Probably a dodecamer composed of six biotin-containing  
 CC alpha subunits and six beta subunits.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; AF310338; AAG50244.1; -  
 DR EMBL; AK007782; BAB25253.1; -  
 DR EMBL; BC021382; AAH21382.1; -  
 DR HSPF; P24182; IDV1.  
 DR MGD; MGI:191289; Mcccl.  
 DR GO; GO:0005759; C:mitochondrial matrix; ISS.

DR GO; GO:0009374; F:biotin binding; ISS.  
 DR GO; GO:0004485; F:methylcrotonyl-CoA carboxylase activity; ISS.  
 DR GO; GO:0006768; P:biotin metabolism; ISS.  
 DR GO; GO:0006552; P:leucine catabolism; ISS.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR InterPro; IPR005482; Biotin\_carb\_C.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR InterPro; IPR005479; CPase\_L\_D2.  
 DR InterPro; IPR005481; CPase\_L\_N.  
 DR Pfam; PF02785; Biotin\_carb\_C; 1.  
 DR Pfam; PF00364; Biotin\_lipoyl; 1.  
 DR Pfam; PF00289; CPase\_L\_chain; 1.  
 DR Pfam; PF02786; CPase\_L\_D2; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 DR PROSITE; PS00867; CPASE; 2; 1. ATP-binding; Transit peptide.  
 KW Mitochondrion; Ligase; Biotin; 1. MITOCHONDRION (POTENTIAL).  
 FT TRANSIT 1 44 METHYLCROTONYL-CoA CARBOXYLASE ALPHA  
 FT CHAIN 45 717 CHAIN.  
 FT NP\_BIND 205 210 ATP (POTENTIAL).  
 FT ACT\_SITE 335 335 BY SIMILARITY.  
 FT BINDING 677 677 BIOTIN (BY SIMILARITY).  
 FT DOMAIN 709 714 POLY-GLU.  
 FT CONFLICT 324 324 R -> K (IN REF. 3).  
 FT CONFLICT 507 507 A -> P (IN REF. 1).  
 SQ SEQUENCE 717 AA; 79343 MW; F653FE7AC1E5AA90 CRC64;  
 Query Match 43.3%; Score 148; DB 1; Length 717;  
 Best Local Similarity 50.0%; Pred. No. 5.8e-07;  
 Matches 28; Conservative 11; Mismatches 17; Indels 0; Gaps 0;  
 QY 1 EGEIPAPLAGT VSKILVKGEDTVKAGQTVLVLEAMKMETEINAPTQKVKVLVKE 56  
 DB 642 QGTTAPMTGTTIEKVFVKAGDRVKAGDSLMVMIAMKWEHTIKAPDGRKKVFSE 697

RESULT 6  
 BCCP STRMU STANDARD; PRT; 130 AA.  
 AC P29337; 1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Biotin carboxyl carrier protein (BCCP).  
 GN BCC OR SMU.1016.  
 OS Streptococcus mutans.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1309;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=UT-041 / Serotype C;  
 RX MEDLINE=93159778; PubMed=8431283;  
 RA Wang D., Weyer M.M., Taricani M., Buckingham K., Sandham H.J.;  
 RT "Biotin-containing protein as a cause of false positive clones in  
 RT gene probing with streptavidin/biotin.";  
 RL Biotechniques 14:209-212 (1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=UA159 / ATCC 700610 / Serotype C;  
 RX MEDLINE=22295063; PubMed=12397186;  
 RA Ajdic D., McGshan W.M., McLaughlin R.E., Savic G., Chang J.,  
 RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,  
 RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;  
 RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental  
 RT pathogen.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).  
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DR EMBL; M80523; AAA03702.1; -.  
 DR EMBL; AE014941; AAN58716.1; -.  
 DR HSSP; P02905; IAE6.  
 DR InterPro; IPR001892; Biotin BS.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR Pfam; PF00364; biotin\_lipoyl; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 KW Fatty acid biosynthesis; Biotin; Complete proteome.  
 FT BINDING 96 96 BIOTIN (BY SIMILARITY).  
 FT CONFLICT 121 121 N -> D (IN REF. 1).  
 SQ SEQUENCE 130 AA; 13600 MW; A0DEA05EC46FF0CB CRC64;

Query Match 42.4%; Score 145; DB 1; Length 130;  
 Best Local Similarity 47.0%; Pred. No. 2.3e-07;  
 Matches 31; Conservative 8; Mismatches 27; Indels 0; Gaps 0;

QY 4 IPAPLAGTSTKILVKGEDTQVLEAMKMETEINAPTDGKVEKLVKRDVQGG 63  
 DB 64 MEAPMPTGILKLVNVGDVSENPMLLEAMKMEIVAGMAGTIVSAIHVSSGQTVMAG 123  
 QY 64 QGLIKI 69  
 DB 124 DNLITI 129

RESULT 7  
 BCCP\_LYCSES STANDARD; PRT; 70 AA.  
 ID BCCP\_LYCSES STANDARD; PRT; 70 AA.  
 AC P05115;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Biotin carrier protein of acetyl-CoA carboxylase (BCCP) (Fragment).  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4081;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RA MEDLINE=87231088; PubMed=3588314;  
 RX Hoffman N.E., Pichersky E., Cahmore A.R.;  
 RT "A tomato cDNA encoding a biotin-binding protein.";  
 RL Nucleic Acids Res. 15:3928-3928(1987).  
 CC -!- FUNCTION: This protein is a component of the acetyl coenzyme A carboxylase complex; first, biotin carboxylase catalyzes the carboxylation of the carrier protein and then the transcarboxylase transfers the carboxyl group to form malonyl-CoA.  
 CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.  
 CC -!- SUBCELLULAR LOCATION: Chloroplast.

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DR EMBL; Y00144; CAA68339.1; -.  
 DR HSSP; P02905; IBD0.  
 DR InterPro; IPR001882; Biotin BS.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR Pfam; PF00364; biotin\_lipoyl; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 KW Fatty acid biosynthesis; Biotin; Chloroplast.  
 FT NON\_TER 1 1  
 FT BINDING 35 35 BIOTIN (BY SIMILARITY).  
 SQ SEQUENCE 70 AA; 7416 MW; D75D018C0BD016BC CRC64;

Query Match 41.8%; Score 143; DB 1; Length 70;  
 Best Local Similarity 48.4%; Pred. No. 2e-07;  
 Matches 30; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 2 GEIPAPLAGTSTKILVKGEDTQVLEAMKMETEINAPTDGKVEKLVKRDVQ 61  
 DB 1 GTVAPVGLGVKLVKDGKVEQGPVLEAMKMEHVKAPANGYVSGLEIKVQSQV 60  
 QY 62 GG 63  
 DB 61 DG 62

RESULT 8  
 MCCA\_HUMAN STANDARD; PRT; 725 AA.  
 ID MCCA\_HUMAN STANDARD; PRT; 725 AA.  
 AC Q96RQ3; Q9H959; Q9NS97;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase alpha subunit).  
 GN MCCC1 OR MCCA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE FROM N.A., AND VARIANTS MCGI ARG-325 AND SER-385.  
 RA PubMed=11170888;  
 RA Gallardo M.E., Desviat L.R., Rodriguez J.M., Eparza-Gordillo J., Portez-Cerda C., Perez B., Rodriguez-Pombo P., Criado O., Sanz R., Morton D.H., Gibson K.M., Le T.P., Ribes A., Rodriguez de Cordoba S., Ugarte M., Penalva M.A.;  
 RA "The molecular basis of 3-methylcrotonylglycinuria, a disorder of leucine catabolism.";  
 RT Am. J. Hum. Genet. 58:334-346(2001).  
 RN [2]

RP SEQUENCE FROM N.A., AND VARIANT HIS-464.  
 RA MEDLINE=21295033; PubMed=11401427;  
 RX Holzinger A., Roeschinger W., Lagler F., Mayerhofer P.U., Lichtner P., Kattenfeld T., Thuy L.P., Nyhan W.L., Koch H.G., Muntau A.C., Roscher A.A.;  
 RA "Human biotin-containing subunit of 3-methylcrotonyl-CoA carboxylase gene (MCCA): cDNA sequence, genomic organization, localization to chromosome band 3q27, and expression.";  
 RL Genomics 72:145-152(2001).  
 RN [3]

RP SEQUENCE FROM N.A., AND VARIANT MCGI PHE-535.  
 RA MEDLINE=21299419; PubMed=11406611;  
 RX Holzinger A., Roeschinger W., Lagler F., Mayerhofer P.U., Lichtner P., Kattenfeld T., Thuy L.P., Nyhan W.L., Koch H.G., Muntau A.C., Roscher A.A.;  
 RA "Cloning of the human MCCA and MCCC genes and mutations therein reveal the molecular cause of 3-methylcrotonyl-CoA: carboxylase deficiency.";  
 RT Hum. Mol. Genet. 10:1299-1306(2001).  
 RN [4]

RP SEQUENCE FROM N.A., AND VARIANTS MCGI VAL-289; SER-385; PRO-437 AND HIS-532.  
 RX PubMed=11181649;  
 RA Baumgartner M.R., Almashanu S., Suormala T., Obie C., Cole R.N., Packman S., Baumgartner E.R., Valle D.;  
 RA "The molecular basis of human 3-methylcrotonyl-CoA carboxylase deficiency.";  
 RT J. Clin. Invest. 107:495-504(2001).  
 RN [5]

RP SEQUENCE FROM N.A.  
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y., Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;

RT "NEDO human cDNA sequencing project."; ;  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 CC -1- CATALYTIC ACTIVITY: ATP + 3-methylcrotonyl-CoA + ADP +  
 CC phosphate + 3-methylglutaconyl-CoA.  
 CC -1- COFACTOR: Biotin.  
 CC -1- PATHWAY: Leucine catabolism.  
 CC -1- SUBUNIT: Probably a dodecamer composed of six biotin-containing  
 CC alpha subunits and six beta subunits.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 CC -1- DISEASE: Defects in MCC1 are the cause of 3-  
 CC methylcrotonylglycinuria type I (MCGI) [MIM:210200]; also  
 CC designated CGA or CG2. MCGI is a recessive disease that is  
 CC characterized by muscular hypotonia and atrophy, probably of  
 CC spinal origin.  
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 CC -----  
 CC EMBL; AF310972; AAG53095.1; -  
 CC EMBL; AB029826; BAA399407.1; -  
 CC EMBL; AF297332; AAK67986.1; -  
 CC EMBL; AF310339; AAG50245.1; -  
 CC EMBL; AK023051; BAB14377.1; -  
 CC EMBL; BC004214; AAH04214.1; -  
 CC EMBL; BC004187; AAH04187.1; -  
 CC GK; Q96R03; -  
 CC MIM; 210200; -  
 CC GO; GO:0005759; C:mitochondrial matrix; NAS.  
 CC GO; GO:000374; F:biotin binding; NAS.  
 CC GO; GO:0004485; F:methylcrotonyl-CoA carboxylase activity; NAS.  
 CC GO; GO:0006768; P:biotin metabolism; NAS.  
 CC GO; GO:0006552; P:leucine catabolism; NAS.  
 CC InterPro; IPR001982; Biotin BS.  
 CC InterPro; IPR005482; Biotin carb C.  
 CC InterPro; IPR000089; Biotin\_lipoyl.  
 CC InterPro; IPR005479; Crase\_L\_D2.  
 CC InterPro; IPR005481; Crase\_L\_N.  
 CC Pfam; PF02785; Biotin carb C; 1.  
 CC Pfam; PF00364; biotin\_lipoyl; 1.  
 CC Pfam; PF00289; CPSase\_L\_Chain; 1.  
 CC Pfam; PF02786; CPSase\_L\_D2; 1.  
 CC PROSITE; PS00188; BIOTIN; 1.  
 CC PROSITE; PS00867; CPSASE\_2; 1.

KW Mitochondrion; Ligase; Biotin; ATP-binding; Transit peptide;  
 KW Disease mutation; Polymorphism.  
 FT TRANSIT 1 47 MITOCHONDRION (POTENTIAL).  
 FT CHAIN 48 725 METHYLCROTONYL-CoA CARBOXYLASE ALPHA  
 FT CHAIN.  
 FT NP BIND 209 214 ATP (POTENTIAL).  
 FT ACT SITE 339 339 BY SIMILARITY.  
 FT BINDING 681 681 BIOTIN (BY SIMILARITY).  
 FT DOMAIN 538 541 POLY-SER.  
 FT DOMAIN 713 718 POLY-GLU.  
 FT VARIANT 289 289 A -> V (in MCGI; mild form).  
 FT VARIANT 325 325 M -> R (in MCGI).  
 FT VARIANT 385 385 R -> S (in MCGI; severe form).  
 FT VARIANT 437 437 L -> P (in MCGI; severe form).  
 FT VARIANT 464 464 P -> H.  
 FT VARIANT 532 532 D -> H (in MCGI; severe form).  
 FT VARIANT 535 535 S -> F (in MCGI; asymptomatic form).  
 FT CONFLICT 469 469 F -> L (in REF. 3 AND 4).  
 SQ SEQUENCE 725 AA; 80433 MW; B847C6B80606B6C0 CRC64;  
 Query Match 41.8%; Score 143; DB 1; Length 725;  
 Best Local Similarity 52.9%; Pred. NO. 1.8e-06;  
 Matches 27; Conservative 10; Mismatches 14; Indels 0; Gaps 0;  
 QY 6 APLAGTVSKILVKEGTVKAGTVLVLEAMKMETEINAPTGDKVEKVLVKE 56  
 DB 651 APTGTIERKVFVKGAGKVGAGDSLWVIAKMEHTIKSPKDGTVKVFYRE 701  
 RESULT 9  
 ID\_MCCA\_ARATH STANDARD; PRT; 734 AA.  
 AC Q42523; Q9S861.  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor  
 DE (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha  
 DE subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase alpha subunit).  
 GN MCCA OR ATL0G3090 OR F1003\_9 OR F1003\_9.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RP [1]  
 RN SEQUENCE FROM N.A. (ISOFORM 2).  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=95232183; PubMed=7716229;  
 RA Weaver L.M., Lebrun L., Franklin A., Huang L., Hoffman N.,  
 RA Wurtele E.S., Nikolau B.J.;  
 RI "Molecular cloning of the biotinylated subunit of 3-methylcrotonyl-  
 RL coenzyme A carboxylase of Arabidopsis thaliana.";  
 RL Plant Physiol. 107:1013-1014 (1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=21016719; PubMed=11130712;  
 RA Treologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
 RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,  
 RA Buehler B., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
 RA Dunn P., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
 RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,  
 RA Gll J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,  
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,  
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,  
RA Pai G., Peterson J.R., Pham P.K., Rizzo M., Rooney T., Rowley D.A.,  
RA Sakano H., Saizberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,  
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,  
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,  
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
RT thaliana";  
RL Nature 408:816-820(2000).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX STRAIN=cv. Columbia;  
RX MEDLINE=22954850; PubMed=14593172;  
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,  
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,  
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,  
RA Miranda M., Quach H.B., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,  
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,  
RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,  
RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.P.,  
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,  
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,  
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,  
RA Satou M., Tambe R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,  
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,  
RT "Empirical analysis of transcriptional activity in the Arabidopsis  
RT genome.";  
RL Science 302:842-846(2003).  
RN [4]  
RP TISSUE SPECIFICITY.  
RP STRAIN=cv. Landsberg erecta, and cv. Columbia;  
RX MEDLINE=20148760; PubMed=10681539;  
RA McKean A.L., Ke J., Song J., Che P., Achenbach S., Nikolau B.J.,  
RA Wurtele E.S.;  
RT "Molecular characterization of the non-biotin-containing subunit of  
RT 3-methylcrotonyl-CoA carboxylase.";  
RL J. Biol. Chem. 275:5582-5590(2000).  
CC -!- CATALYTIC ACTIVITY: ATP + 3-methylcrotonyl-CoA + HCO(3) (-) = ADP +  
CC phosphate + 3-methylglutaconyl-CoA.  
CC -!- COFACTOR: Biotin.  
CC -!- PATHWAY: Leucine catabolism.  
CC -!- SUBUNIT: Probably a heterodimer composed of biotin-containing  
CC alpha subunits and beta subunits (By similarity).  
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q42523-1; Sequences=Displayed;  
CC Name=2;  
CC IsoId=Q42523-2; Sequences=VSP 008910;  
CC Note=May be due to an exon skipping. No experimental  
CC confirmation available;  
CC -!- TISSUE SPECIFICITY: In roots, cotyledons, leaves, flowers,  
CC ovaries, siliques and embryos.  
CC -!- MISCELLANEOUS: Temporal and spatial accumulation of the alpha and  
CC beta subunits during development at approximately equal molar  
CC ratios.  
CC -!- CAUTION: Ref.2 sequence differs from that shown due to erroneous  
CC gene model prediction.  
CC -----  
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CC -----  
CC EMBL: U12536; AAA67356.1;  
CC EMBL: AC008550; AAD28600.1; ALT\_SEQ.  
CC EMBL: AY070723; AAL50065.1; -.

DR HSSP; P24182; 1BNC.  
DR InterPro; IPR001882; Biotin\_BS.  
DR InterPro; IPR005482; Biotin\_carb C.  
DR InterPro; IPR000089; Biotin\_lipoYL.  
DR InterPro; IPR005479; CPhase\_L\_D2.  
DR InterPro; IPR005481; CPhase\_L\_N.  
DR Pfam; PF02785; Biotin\_carb C; 1.  
DR Pfam; PF02785; Biotin\_lipoYL; 1.  
DR Pfam; PF02786; CPhase\_L\_D2; 1.  
DR Pfam; PF02786; CPhase\_L\_N; 1.  
DR PROSITE; PS00188; BIOTIN; 1.  
DR PROSITE; PS00866; CPhase\_L; 1.  
DR PROSITE; PS00867; CPhase\_2; 1.  
KW Ligase; Mitochondrion; ATP-binding; Biotin; Transit peptide;  
KW Alternative splicing.  
FT TRANSIT 1 25 MITOCHONDRION (POTENTIAL).  
FT CHAIN 26 734 METHYLCROTONYL-CoA CARBOXYLASE ALPHA  
FT CHAIN.  
FT NP\_BIND 198 203 ATP (POTENTIAL).  
FT ACT\_SITE 329 329 BY SIMILARITY.  
FT BINDING 699 699 BIOTIN (BY SIMILARITY).  
FT VARSPIC 281 300 Missing (in isoform 2).  
FT /FTid=VSP\_008910.  
FT CONFLICT 85 85 V -> D (IN REF. 1).  
FT CONFLICT 92 92 A -> AK (IN REF. 1).  
FT CONFLICT 430 430 W -> L (IN REF. 1).  
SQ SEQUENCE 734 AA; 80451 MW; 251CACF6464B046B CRC64;  
Query Match 41.8%; Score 143; DB 1; Length 734;  
Best Local Similarity 45.6%; Pred. No. 1.8e-06;  
Matches 31; Conservative 10; Mismatches 27; Indels 0; Gaps 0;  
QY 2 GEIPAPLAGTISKILVKEGDTVKAGQTVLVLEAMKMETEINAPDGVKVKLVKRDVQ 61  
DB 665 GTIVAPAGLVVVKVLENEAKVDQGVILVLEAMKMEHVVKAPSSGSIQDLKVKAGQVS 724  
QY 62 GQGLIKI 69  
DB 725 DGSALFRI 732  
RESULT 10  
ID PYCB METH STANDARD; PRT; 569 AA.  
AC 027179;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Pyruvate carboxylase subunit B (EC 6.4.1.1) (Pyruvic carboxylase B).  
OS PYCB OR MTH1107.  
OS Methanobacterium thermoautotrophicum.  
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;  
OC Methanobacteriaceae; Methanothermobacter.  
OX NCBI\_TaxID=187420;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=Delta H;  
RX MEDLINE=98037514; PubMed=9371463;  
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,  
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,  
RA Harrison D., Hoang L., Kiegler P., Lumm W., Pothier B., Qiu D.,  
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,  
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,  
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;  
RT "Complete genome sequence of Methanobacterium thermoautotrophicum  
RT deltaH: functional analysis and comparative genomics.";  
RL J. Bacteriol. 179:7135-7155(1997).  
RN [2]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.  
RX STRAIN=Delta H;  
RX MEDLINE=98148063; PubMed=9478969;  
RA Mukhopadhyay B., Stoddard S.F., Wolfe R.S.;





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CC DR EMBL; J03889; AAA34843.1; -.
CC DR EMBL; J27584; CAA96765.1; -.
CC DR PIR; S64066; QYBYP.
CC DR HSSP; P24182; 1BNC.
CC DR GerMOnline; 141110; -.
CC DR SGD; S0003030; PYCL.
CC DR GO; GO:0005829; C:cytosol; IDA.
CC DR GO; GO:0004736; F:pyruvate carboxylase activity; IDA.
CC DR InterPro; IPR001882; Biotin_BS.
CC DR InterPro; IPR005482; Biotin carb C.
CC DR InterPro; IPR000089; Biotin lipoyl.
CC DR InterPro; IPR005479; Cbase_L_D2.
CC DR InterPro; IPR005481; Cbase_L_N.
CC DR InterPro; IPR000891; HMGL-like.
CC DR InterPro; IPR003379; PYC_OADA.
CC DR Pfam; PF02785; Biotin carb C; 1.
CC DR Pfam; PF00364; biotin lipoyl; 1.
CC DR Pfam; PF00289; Cbase_L chain; 1.
CC DR Pfam; PF02786; Cbase_L_D2; 1.
CC DR Pfam; PF00682; HMGL-like; 1.
CC DR Pfam; PF02436; PYC_OADA; 1.
CC DR TIGRFAMs; TIGR01235; pyruv carbox; 1.
CC DR PROSITE; PS00188; BIOTIN; 1.
CC DR PROSITE; PS00866; CPSASE_1; 1.
CC DR PROSITE; PS00867; CPSASE_2; 1.
CC DR LGase; Multifunctional enzyme; Biotin; Gluconeogenesis; ATP-binding;
CC DR Zinc; Multigene family.
CC FT NP_BIND 182 187 ATP (POTENTIAL).
CC FT ACT_SITE 312 312 BY SIMILARITY.
CC FT BINDING 1135 1135 BIOTIN (BY SIMILARITY).
CC FT CONFLICT 462 462 T -> G (IN REF. 1).
CC FT CONFLICT 493 493 V -> D (IN REF. 1).
CC FT CONFLICT 595 595 R -> A (IN REF. 1).
CC FT CONFLICT 619 619 E -> Q (IN REF. 1).
CC FT CONFLICT 664 664 G -> S (IN REF. 1).
CC FT CONFLICT 772 772 A -> R (IN REF. 1).
CC FT CONFLICT 879 879 E -> Q (IN REF. 1).
CC FT CONFLICT 909 909 Q -> K (IN REF. 1).
CC SQ SEQUENCE 1178 AA; 130099 MW; BC7110A8AFB23E04 CRC64;

Query Match 38.9%; Score 133; DB 1; Length 1178;
Best Local Similarity 42.2%; Pred. No. 2.6e-05;
Matches 27; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

QY 4 IPAPLAGTVSKLVKGGTVKAGTVLVLEAMKMETEINAPTDGKVEKLVKERDAYOGG 63
Db 1103 IGAPMAGVIVEVKVHKGSLIKKGPVAVLSAMKMEIISPSDQKVEVFSVSGENVDS 1162
QY 64 QGLI 67
Db 1163 DLLV 1166

RESULT 14
PVC_PICPA STANDARD; PRT; 1189 AA.
AC P78992;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Pyruvate carboxylase (EC 6.4.1.1) (Pyruvic carboxylase) (PCB).
GN PYCL.
OS Pichia pastoris (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4922;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98301182; PubMed=9639311;
RA Menendez J., Delgado J., Gancedo C.;
RT "Isolation of the Pichia pastoris PYCL gene encoding pyruvate

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carboxylase and identification of a suppressor of the pyc
phenotype."
RL Yeast 14:647-654 (1998).
CC -!- FUNCTION: Pyruvate carboxylase catalyzes a 2-step reaction,
CC involving the ATP-dependent carboxylation of the covalently
CC attached biotin in the first step and the transfer of the
CC carboxyl group to pyruvate in the second (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3) (-) = ADP + phosphate +
CC oxaloacetate.
CC -!- COFACTOR: Biotin and zinc.
CC -!- PATHWAY: Gluconeogenesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
CC AND CARBAMYL PHOSPHATE SYNTHETASES.
CC
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CC
CC EMBL; Y11106; CAA71993.1; -.
CC HSSP; P24182; 1DV1.
CC InterPro; IPR001882; Biotin_BS.
CC InterPro; IPR005482; Biotin carb C.
CC InterPro; IPR000089; Biotin lipoyl.
CC InterPro; IPR005483; Cbase_L.
CC InterPro; IPR005479; Cbase_L_D2.
CC InterPro; IPR005481; Cbase_L_N.
CC InterPro; IPR000891; HMGL-like.
CC InterPro; IPR003379; PYC_OADA.
CC InterPro; IPR005930; Pyruv carbox.
CC Pfam; PF02785; Biotin carb C; 1.
CC Pfam; PF00364; biotin lipoyl; 1.
CC Pfam; PF00289; Cbase_L chain; 1.
CC Pfam; PF02786; Cbase_L_D2; 1.
CC Pfam; PF00682; HMGL-like; 1.
CC Pfam; PF02436; PYC_OADA; 1.
CC PRINTS; PR00098; CFSASE.
CC TIGRFAMs; TIGR01235; pyruv carbox; 1.
CC PROSITE; PS00188; BIOTIN; 1.
CC PROSITE; PS00866; CPSASE_1; 1.
CC PROSITE; PS00867; CPSASE_2; 1.
CC LGase; Multifunctional enzyme; Biotin; Gluconeogenesis; ATP-binding;
CC Zinc.
CC NP_BIND 185 190 ATP (POTENTIAL).
CC ACT_SITE 315 315 BY SIMILARITY.
CC BINDING 1140 1140 BIOTIN (BY SIMILARITY).
CC SEQUENCE 1189 AA; 131400 MW; 8B6E858079657914 CRC64;

Query Match 38.8%; Score 132; DB 1; Length 1189;
Best Local Similarity 46.6%; Pred. No. 3.2e-05;
Matches 27; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

QY 3 EIPAPLAGTVSKLVKGGTVKAGTVLVLEAMKMETEINAPTDGKVEKLVKERDAY 60
Db 1107 EIGAPMAGVVVVRVHENGVEVKKGDPVAVLSAMKMEVISSPVAGRVGIATKENDSV 1164

RESULT 15
BCCA_MYCLE STANDARD; PRT; 598 AA.
AC P46392;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acetyl-/propionyl-coenzyme A carboxylase alpha chain [includes: Biotin
DE carboxylase (EC 6.3.4.14); Biotin carboxyl carrier protein (BCCP)].
GN BCCA OR ML0726 OR B1308_C1_129.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

```

CC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1169;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94222829; PubMed=7909542;  
 RA Norman E., de Smet K.A.L., Stoker N.G., Ratledge C., Wheeler P.R.,  
 RA Dale J.W.;  
 RT "Lipid synthesis in mycobacteria: characterization of the biotin  
 RT carboxyl carrier protein genes from Mycobacterium leprae and M.  
 RL J. Bacteriol. 176:2525-2531(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Smith D.R., Robison K.;  
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TN;  
 RX MEDLINE=21128732; PubMed=11234002;  
 RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,  
 RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,  
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,  
 RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,  
 RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,  
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,  
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,  
 RA Barrall B.G.;  
 RT "Massive gene decay in the leprosy bacillus."  
 RL Nature 409:1007-1011(2001).  
 CC -!- FUNCTION: THIS PROTEIN CARRIES TWO FUNCTIONS: BIOTIN CARBOXYL  
 CC CARRIER PROTEIN AND BIOTIN CARBOXYLTRANSFERASE  
 CC -!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)  
 CC = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.  
 CC -!- COFACTOR: Biotin.  
 CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.  
 CC -!- SUBUNIT: MULTIMER COMPRISED OF 2 DIFFERENT SUBUNITS, THE LARGER  
 CC ONE (63/64 kDa) HAS BIOTIN CARBOXYLASE AND BIOTIN CARRIER  
 CC FUNCTIONS, WHILE THE SMALLER SUBUNIT POSSESSES CARBOXYLTRANSFERASE  
 CC AND SUBSTRATE BINDING ACTIVITY.  
 CC -!- SIMILARITY: TO OTHER BIOTIN-DEPENDENT ENZYMES AND CARBAMOYL-  
 CC PHOSPHATE SYNTHETASES.  
 CC -----  
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 CC -----  
 CC EMBL; X63470; CAN45070.1; -;  
 CC EMBL; U00012; AAA85920.1; -;  
 CC EMBL; AL583919; CAC30235.1; -;  
 CC PIR; A55579; A55579.  
 CC PIR; G86999; G86999.  
 CC HSSP; P24182; 1BNC.  
 CC Leproma; M0726; -;  
 CC InterPro; IPR001882; Biotin\_BS.  
 CC InterPro; IPR005482; Biotin\_carb\_C.  
 CC InterPro; IPR000089; Biotin\_lipoyl.  
 CC InterPro; IPR005479; CPase\_L\_D2.  
 CC InterPro; IPR005481; CPase\_L\_N.  
 CC Pfam; PF02785; Biotin\_carb\_C; 1.  
 CC Pfam; PF03664; biotin\_lipoyl; 1.  
 CC Pfam; PF0289; CPase\_L\_chain; 1.  
 CC Pfam; PF02786; CPase\_L\_D2; 1.  
 CC PROSITE; PS00188; BIOTIN; 1.  
 CC PROSITE; PS00866; CPASE\_1; 1.  
 CC PROSITE; PS00867; CPASE\_2; 1.  
 CC Fatty acid biosynthesis; Ligase; Biotin; Multifunctional enzyme;  
 CC ATP-binding; Complete proteome.  
 CC DOMAIN 11 441 BIOTIN CARBOXYLASE.  
 CC -----

FT DOMAIN 532 598 BIOTIN CARBOXYL CARRIER PROTEIN.  
 FT NP\_BIND 169 174 ATP (BY SIMILARITY).  
 FT BINDING 299 299 BY SIMILARITY.  
 FT BINDING 564 564 BIOTIN (BY SIMILARITY).  
 FT CONFLICT 30 30 D -> H (IN REF. 1).  
 SQ SEQUENCE 598 AA; 63863 MW; 5F2E291D7C54515D CRC64;  
 Query Match 38.0%; Score 130; DB 1; Length 598;  
 Best Local Similarity 43.9%; Pred. No. 2.7e-05;  
 Matches 29; Conservative 10; Mismatches 27; Indels 0; Gaps 0;  
 QY 4 IPAPLAGTVSKILVKEGTVKAGQTVLVLEAMKMETEINAPTQGVKVKLVKRDVQGG 63  
 Db 532 VTAPMQSTVVKVAVAEQTVWGLVVLVLEAMKMNENPTAKHKGIIITGLAVEAGTAITQG 591  
 QY 64 QGLIKI 69  
 Db 592 TVLAEI 597

RESULT 16  
 MCCA SOYBN  
 ID MCCA SOYBN STANDARD; PRT; 731 AA.  
 AC Q42777; Q42778;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor  
 DE (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCase alpha  
 DE subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase alpha subunit).  
 GN MCCA.  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 OX NCBI\_TaxID=3847;  
 RN [1]  
 RP SEQUENCE FROM N.A. AND SEQUENCE OF N-TERMINUS.  
 RC STRAIN=cv. Corsey 79; TISSUE=Cotyledon;  
 RX MEDLINE=94286521; PubMed=8016064;  
 RA Song J., Wurtele E.S., Nikolau B.J.;  
 RT "Molecular cloning and characterization of the cDNA coding for the  
 RT biotin-containing subunit of 3-methylcrotonyl-CoA carboxylase:  
 RT identification of the biotin carboxylase and biotin-carrier  
 RT domains."  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:5779-5783(1994).  
 CC -!- CATALYTIC ACTIVITY: ATP + 3-methylcrotonyl-CoA + HCO(3) (-) = ADP +  
 CC phosphate + 3-methylglutaconyl-CoA.  
 CC -!- COFACTOR: Biotin.  
 CC -!- PATHWAY: Leucine catabolism.  
 CC -!- SUBUNIT: Probably a heterodimer composed of biotin-containing  
 CC alpha subunits and beta subunits (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 CC -!- TISSUE SPECIFICITY: In leaves, cotyledons and stems.  
 CC -----  
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 CC -----  
 CC EMBL; U08469; AAA53140.1; -;  
 CC EMBL; U08846; AAA53141.1; -;  
 CC PIR; T06361; T06360.  
 CC HSSP; P24182; 1BNC.  
 CC InterPro; IPR001882; Biotin\_BS.  
 CC InterPro; IPR005482; Biotin\_carb\_C.  
 CC InterPro; IPR000089; Biotin\_lipoyl.  
 CC InterPro; IPR005479; CPase\_L\_D2.  
 CC InterPro; IPR005481; CPase\_L\_N.  
 CC Pfam; PF02785; Biotin\_carb\_C; 1.  
 CC Pfam; PF03664; biotin\_lipoyl; 1.  
 CC Pfam; PF0289; CPase\_L\_chain; 1.  
 CC Pfam; PF02786; CPase\_L\_D2; 1.  
 CC PROSITE; PS00188; BIOTIN; 1.  
 CC PROSITE; PS00866; CPASE\_1; 1.  
 CC PROSITE; PS00867; CPASE\_2; 1.  
 CC Fatty acid biosynthesis; Ligase; Biotin; Multifunctional enzyme;  
 CC ATP-binding; Complete proteome.  
 CC DOMAIN 11 441 BIOTIN CARBOXYLASE.  
 CC -----







```

CC -|- COPACTOR: Biotin.
CC -|- PATHWAY: Long-chain fatty acid biosynthesis; first step.
CC -|- SUBUNIT: MULTIMER COMPRISED OF 2 DIFFERENT SUBUNITS, THE LARGER
CC ONE (63/64 kDa) HAS BIOTIN CARBOXYLASE AND BIOTIN CARRIER
CC FUNCTIONS, WHILE THE SMALLER SUBUNIT POSSESSES CARBOXYLTRANSFERASE
CC AND SUBSTRATE BINDING ACTIVITY.
CC -|- SIMILARITY: TO OTHER BIOTIN-DEPENDENT ENZYMES AND CARBAMOYL-
CC PHOSPHATE SYNTHETASES.
CC
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CC
CC -----
CC EMBL: Z19549; CAA79609.1; -.
CC EMBL: Z95556; CAB08919.1; -.
CC EMBL: AE007094; AAK46880.1; -.
CC EMBL: BX248342; CAD97390.1; -.
CC PIR: B55579; B55579.
CC HSSP: P24182; IBNC.
CC TIGR: MT2576; -.
CC TubercuList: Rv2501c; -.
CC InterPro: IPR001882; Biotin_BS.
CC InterPro: IPR005482; Biotin_carb_C.
CC InterPro: IPR000089; Biotin_lipoyl.
CC InterPro: IPR005479; CPhase_L_D2.
CC InterPro: IPR005481; CPhase_L_N.
CC Pfam: PF02785; Biotin_carb_C; 1.
CC Pfam: PF00364; biotin_lipoyl; 1.
CC Pfam: PF00289; CPhase_L_chain; 1.
CC Pfam: PF02786; CPhase_L_D2; 1.
CC PROSITE: PS00188; BIOTIN; 1.
CC PROSITE: PS00866; CPSASE; 1; 1.
CC PROSITE: PS00867; CPSASE; 2; 1.
CC Fatty acid biosynthesis; Ligase; Biotin; Multifunctional enzyme;
CC ATP-binding; Complete proteome.
CC
CC DOMAIN 1 437 BIOTIN CARBOXYLASE.
CC DOMAIN 588 654 BIOTIN CARBOXYL CARRIER PROTEIN.
CC NP_BIND 162 167 ATP (BY SIMILARITY).
CC ACT_SITE 294 294 BY SIMILARITY.
CC BINDING 520 620 BIOTIN (BY SIMILARITY).
CC SEQUENCE 654 AA; 70592 MW; FA0ALAL46432CAF CRC64;
CC
CC Query Match 36.4%; Score 124.5; DB 1; Length 654;
CC Best Local Similarity 41.8%; Pred. No. 9.8e-05;
CC Matches 28; Conservative 14; Mismatches 24; Indels 1; Gaps 1;
CC
CC Qy 3 BIPAPLAGTSKILVKGSDTVKAGQTVLVLEAMKMETEINAPTCKVEKVLKRDVQV 62
CC Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC Qy 63 GQGLIKI 69
CC Db 646 EQVLARI 652
CC
CC RESULT 20
CC BCCP CHLTR STANDARD; PRT; 164 AA.
CC AC 084125;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 26-OCT-2001 (Rel. 40, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP).
CC GN ACCB OR Crl23
CC OS Chlamydia trachomatis.
CC OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
CC OX NCBI_TaxID=813;
CC RN [1]
CC RP SEQUENCE FROM N.A.

```

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RC STRAIN=D/UW-3/Cx;
RX MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kaiman S., Lammell C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.";
RL Science 282:754-759(1998).
CC -|- FUNCTION: This protein is a component of the acetyl coenzyme A
CC carboxylase complex; first, biotin carboxylase catalyzes the
CC carboxylation of the carrier protein and then the transcarboxylase
CC transfers the carboxyl group to form malonyl-CoA (By similarity).
CC -|- PATHWAY: Long-chain fatty acid biosynthesis; first step.
CC -|- SUBUNIT: Homodimer (By similarity).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL: AE001286; AAC67714.1; -.
CC PIR: G71553; G71553.
CC HSSP: P02905; 3BDO.
CC PHCI-2DPAGE; O84125; -.
CC InterPro: IPR001249; AccoA_biotinCC.
CC InterPro: IPR001882; Biotin_BS.
CC InterPro: IPR000089; Biotin_lipoyl.
CC Pfam: PF00364; biotin_lipoyl; 1.
CC PRINTS: PR01071; AC0ABIOTINGC.
CC TIGR: TIGR00531; BCCP; 1.
CC PROSITE: PS00188; BIOTIN; 1.
CC Fatty acid biosynthesis; Biotin; Complete proteome.
CC BINDING 128 128 BIOTIN (BY SIMILARITY).
CC SEQUENCE 164 AA; 18198 MW; BD0BA4CEB2D384C CRC64;
CC
CC Query Match 35.7%; Score 122; DB 1; Length 164;
CC Best Local Similarity 36.1%; Pred. No. 4.7e-05;
CC Matches 30; Conservative 11; Mismatches 28; Indels 14; Gaps 2;
CC
CC Qy 1 EGEIPA-----PLAGTV-----SKLVKSGDTVKAGQTVLVLEAMKMETEINAPT 46
CC Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC Qy 47 GKVEKVLKRDVAVQGGGLIKI 69
CC Db 139 GRVEEILITNGDPVQFGSKLFRI 161
CC
CC RESULT 21
CC PYC_HUMAN STANDARD; PRT; 1178 AA.
CC AC P11498; Q16705;
CC DT 01-OCT-1989 (Rel. 12, Created)
CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Pyruvate carboxylase, mitochondrial precursor (EC 6.4.1.1) (Pyruvic
CC carboxylase) (PCB).
CC GN PC.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC OX NCBI_TaxID=9606;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE=Kidney, and Liver;
CC RX MEDLINE=95002202; PubMed=7918683;
CC RA Wexler I.D., Du Y., Lisgaris M.V., Mandal S.K., Freytag S.O.,
CC Yang B.-S., Liu T.-C., Kwon M., Patel M.S., Kerr D.S.;
CC "Primary amino acid sequence and structure of human pyruvate
CC carboxylase.";

```

RL Biochim. Biophys. Acta 1227:46-52 (1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=94324922; PubMed=8048912;  
 RA Mackay N., Rigat B., Douglas C., Chen H.S., Robinson B.H.;  
 RT "cDNA cloning of human kidney pyruvate carboxylase.";  
 RL Biochem. Biophys. Res. Commun. 202:1009-1014 (1994).  
 [3]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Kidney, and Liver;  
 RC Walker M.E., Jirapakdee S., Val D.L., Wallace J.C.;  
 RA Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Lung;  
 RC MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Griewood J., Schmutz J., Myers R.M.,  
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [5]  
 RN SEQUENCE OF 1083-1178 FROM N.A.  
 RP MEDLINE=87212051; PubMed=3555348;  
 RX Lanhonwah A.-M., Quan F., Gravel R.A.;  
 RA "Sequence homology around the biotin-binding site of human propionyl-  
 RT CoA carboxylase and pyruvate carboxylase.";  
 RL Arch. Biochem. Biophys. 254:631-636 (1987).  
 [6]  
 RN SEQUENCE OF 1135-1178 FROM N.A.  
 RP MEDLINE=85030380; PubMed=6548474;  
 RX Freytag S.O., Collier K.J.;  
 RA "Molecular cloning of a cDNA for human pyruvate carboxylase.  
 RT Structural relationship to other biotin-containing carboxylases and  
 RT regulation of mRNA content in differentiating preadipocytes.";  
 RL J. Biol. Chem. 259:12831-12837 (1984).  
 [7]  
 RN VARIANTS PC DEFICIENCY THR-610 AND ILE-743.  
 RP MEDLINE=98254451; PubMed=9585612;  
 RX Carbone M.A., Mackay N., Ling M., Cole D.E.C., Douglas C., Rigat B.,  
 RA Feigenbaum A., Clarke J.T.R., Haworth J.C., Greenberg C.R.,  
 RA Seargeant L., Robinson B.H.;  
 RT "American pyruvate carboxylase deficiency is associated with two  
 RT distinct missense mutations.";  
 RL Am. J. Hum. Genet. 62:1312-1319 (1998).  
 [8]  
 RN VARIANTS PC DEFICIENCY ALA-145 AND CYS-451.  
 RX MEDLINE=98244401; PubMed=9585002;  
 RA Wexler I.D., Kerr D.S., Du Y., Kaung M.M., Stephenson W., Lusk M.M.,  
 RA Wapner R.S., Higgins J.J.;  
 RT "Molecular characterization of pyruvate carboxylase deficiency in two  
 RT consanguineous families.";  
 RL Pediatr. Res. 43:579-584 (1998).  
 CC -!- FUNCTION: Pyruvate carboxylase catalyzes a 2-step reaction,  
 CC involving the ATP-dependent carboxylation of the covalently  
 CC attached biotin in the first step and the transfer of the  
 CC carboxyl group to pyruvate in the second. Catalyzes in a tissue

specific manner, the initial reactions of glucose (liver, kidney) and lipid (adipose tissue, liver, brain) synthesis from pyruvate.  
 -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3) (-) = ADP + phosphate + oxaloacetate.  
 -!- COFACTOR: Biotin and manganese.  
 -!- PATHWAY: Gluconeogenesis and lipogenesis.  
 -!- SUBUNIT: Homotrimer.  
 -!- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 -!- DISEASE: Defects in PC are the cause of pyruvate carboxylase deficiency (PC deficiency) [MIM:266150]. PC deficiency leads to lactic acidosis, mental retardation and death. It occurs in three forms: mild or type A, severe neonatal or type B, and a very mild lacticacidemia.  
 -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES AND CARBAMYL PHOSPHATE SYNTHETASES.

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EMBL; U04641; AAA99537.1; -  
 EMBL; S72370; AAB31500.1; -  
 EMBL; U30891; AAB82937.1; -  
 EMBL; BC011617; AAH11617.1; -  
 EMBL; M26122; AAA84233.1; -  
 EMBL; K02282; AAA60033.1; -  
 PIR; G01933; JC2460.  
 HSPP; P24182; 1BNC.  
 Genew; HGNC:8636; PC.  
 GK; P11498; -  
 MIM; 266150; -  
 GO; GO:0005524; F:ATP binding; TAS.  
 GO; GO:0009374; F:biotin binding; TAS.  
 GO; GO:0004736; F:pyruvate carboxylase activity; TAS.  
 InterPro; IPR01882; Biotin\_B8.  
 InterPro; IPR005482; Biotin\_carb\_C.  
 InterPro; IPR000089; Biotin\_lipoyl.  
 InterPro; IPR003479; CPase\_L\_D2.  
 InterPro; IPR005481; CPase\_L\_N.  
 InterPro; IPR000891; HMGL-like.  
 InterPro; IPR003379; PYC\_OADA.  
 InterPro; IPR005930; Pyruv\_carbox.  
 Pfam; PF02785; Biotin\_carb\_C; 1.  
 Pfam; PF00364; biotin\_lipoyl; 1.  
 Pfam; PF00289; CPase\_L\_chain; 1.  
 Pfam; PF02786; CPase\_L\_D2; 1.  
 Pfam; PF00682; HMGL-like; 1.  
 Pfam; PF02436; PYC\_OADA; 1.  
 TIGRfam; TIGR01235; pyruv\_carbox; 1.  
 PROSITE; PS00188; BIOTIN; 1.  
 Ligase; Multifunctional enzyme; Biotin; Manganese; Gluconeogenesis; ATP-binding; Mitochondrion; Lipid synthesis; Transit peptide; Disease mutation.

TRANSIT	1	20	MITOCHONDRION (POTENTIAL).
CHAIN	21	1178	PYRUVATE CARBOXYLASE.
DOMAIN	21	549	BIOTIN CARBOXYLASE (BY SIMILARITY).
DOMAIN	550	1000	CARBOXYLTRANSFERASE (BY SIMILARITY).
DOMAIN	1096	1178	BIOTIN CARBOXYL CARRIER PROTEIN (BY SIMILARITY).
NP_BIND	198	203	ATP (BY SIMILARITY).
ACT_SITE	328	328	BY SIMILARITY.
BINDING	1144	1144	BIOTIN (BY SIMILARITY).
VARIANT	145	145	V -> A (in PC deficiency; mild). R -> C (in PC deficiency; mild). /FTid=VAR_015199. /FTid=VAR_015200. A -> T (in PC deficiency; mild). /FTid=VAR_008095. M -> I (in PC deficiency; mild).
VARIANT	451	451	
VARIANT	610	610	
VARIANT	743	743	

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FT CONFLICT 225 226 /FTID=VAR_008096:
FT CONFLICT 352 352 LA -> WP (IN REF. 2).
FT CONFLICT 352 352 A -> S (IN REF. 3).
FT CONFLICT 386 386 RS -> PT (IN REF. 2).
FT CONFLICT 486 486 EL -> DV (IN REF. 2).
FT CONFLICT 638 638 P -> R (IN REF. 2).
FT CONFLICT 729 729 E -> A (IN REF. 2).
FT CONFLICT 774 775 DT -> AP (IN REF. 2).
SQ SEQUENCE 1178 AA; 129633 MW; 381F527553A20095 CRC64;

Query Match
Best Local Similarity 35.4%; Score 121; DB 1; Length 1178;
Matches 28; Conservative 13; Mismatches 28; Indels 0; Gaps 0;

Qy 1 EGEIPAPLAGTVSKILVKEGDTVAGQTVLVLEAMKMETEINAPTDSKVKLVKRDV 60
Db 1109 KGQIGAPMPGKVIDIKVAGAKVAGQPLCVLSAMKMETVTVTSMEGTIRKRVHTKMTL 1168
Qy 61 QGGQGLIKI 69
Db 1169 EGGDLILEI 1177

RESULT 22
PVC_RAT
ID_PVC_RAT STANDARD; PRT; 1178 AA.
AC P2873; Q6455;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pyruvate carboxylase, mitochondrial precursor (EC 6.4.1.1) (Pyruvic
GN carboxylase) (PCB).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Liver;
RA MEDLINE=96096548; PubMed=8522203;
RA Lehn D.A., Moran S.M., Macdonald M.J.;
RT "The sequence of the rat pyruvate carboxylase-encoding cDNA.";
RL Gene 165:331-332 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Liver;
RA MEDLINE=96257760; PubMed=8687410;
RA Jitrapakdee S., Booker G.W., Cassidy A.I., Wallace J.C.;
RT "Cloning, sequencing and expression of rat liver pyruvate
carboxylase.";
RL Biochem. J. 316:631-637 (1996).
CC -!- FUNCTION: Pyruvate carboxylase catalyzes a 2-step reaction,
involving the ATP-dependent carboxylation of the covalently
attached biotin in the first step and the transfer of the carboxyl
group to pyruvate in the second. Catalyzes in a tissue specific
manner, the initial reactions of glucose (liver, kidney) and lipid
(adipose tissue, liver, brain) synthesis from pyruvate.
CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
oxaloacetate.
CC -!- COFACTOR: Biotin and manganese (By similarity).
CC -!- PATHWAY: Gluconeogenesis and lipogenesis.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
AND CARBAMYL PHOSPHATE SYNTHASES.

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CC
DR EMBL; U2334; AAA96256.1; -
DR EMBL; U36585; AAC52668.1; -
DR PIR; S68252; JC4391.
DR HSSP; P24182; 1BNC.
DR InterPro; IPR001882; Biotin BS.
DR InterPro; IPR005482; Biotin Carb C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC OADA.
DR InterPro; IPR005930; Pyruv carbox.
DR Pfam; PF02785; Biotin carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPase_L_chain; 1.
DR Pfam; PF02786; CPase_L_D2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC OADA; 1.
DR TIGRFAMs; TIGR01235; Pyruv carbox; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Ligase; Multifunctional enzyme; Biotin; Manganese; Gluconeogenesis;
KW ATP-binding; Mitochondrion; Lipid synthesis; Transit peptide.
FT TRANSIT 1 20 MITOCHONDRION (POTENTIAL).
FT CHAIN 21 1178 PYRUVATE CARBOXYLASE.
FT DOMAIN 21 549 BIOTIN CARBOXYLASE (BY SIMILARITY).
FT DOMAIN 550 1000 CARBOXYLTRANSFERASE (BY SIMILARITY).
FT DOMAIN 1096 1178 BIOTIN CARBOXYL CARRIER PROTEIN
(BY SIMILARITY).
FT NP_BIND 198 203 ATP (BY SIMILARITY).
FT ACT_SITE 328 328 BY SIMILARITY.
FT BINDING 1144 1144 BIOTIN (BY SIMILARITY).
FT CONFLICT 222 222 P -> S (IN REF. 2).
FT CONFLICT 866 866 D -> I (IN REF. 2).
FT CONFLICT 977 977 G -> R (IN REF. 2).
SQ SEQUENCE 1178 AA; 129689 MW; 855FA19BC132A8DD CRC64;

Query Match
Best Local Similarity 34.8%; Score 119; DB 1; Length 1178;
Matches 28; Conservative 15; Mismatches 28; Indels 0; Gaps 0;

Qy 1 EGEIPAPLAGTVSKILVKEGDTVAGQTVLVLEAMKMETEINAPTDSKVKLVKRDV 60
Db 1109 KGQIGAPMPGKVIDIKVAGAKVAGQPLCVLSAMKMETVTVTSMEGTIRKRVHTKMTL 1168
Qy 61 QGGQGLIKI 69
Db 1169 EGGDLILEI 1177

RESULT 23
BTB7_MYCSM
ID_BT7_MYCSM STANDARD; PRT; 70 AA.
AC Q9XCD6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Biotinylated protein TB7.3 homolog.
OS Mycobacterium smegmatis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1772;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 700084 / mc(2)155;
RX MEDLINE=99328972; PubMed=10400584;
RA Fernandes N.D., Wu Q.-L., Kong D., Puyang X., Garg S., Husson R.N.;
RT "A mycobacterial extracytoplasmic sigma factor involved in survival
following heat shock and oxidative stress.";
RL J. Bacteriol. 181:4266-4274 (1999).
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EMBL; U47920; AAC45354.1; -
EMBL; AB004914; AAG038401.1; -
PIR; H83018; H83018.
HSSP; P10802; LEAF.
InterPro; IPR001078; 2Oxoacid_dh.
InterPro; IPR006256; AceP.
InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR004167; E3_binding.
InterPro; IPR003016; Lipoyl_BS.
Pfam; PF001198; 2-oxoacid_dh; 1.
Pfam; PF00364; biotin_lipoyl; 2.
Pfam; PF02817; e3_binding; 1.
ProDom; PD001115; 2Oxoacid_dh; 1.
TIGRFAMs; TIGR01348; PDHac_trif_long; 1.
PROSITE; PS00189; LIPOYL; 2.
Glycolysis; Transferrase; Acyltransferase; Repeat; Lipoyl;
Complete proteome.
FT BINDING 41 LIPOYL (BY SIMILARITY).
FT BINDING 159 LIPOYL (BY SIMILARITY).
FT ACT_SITE 520 POTENTIAL.
FT CONFLICT 225 A -> V (IN REF. 1).
FT CONFLICT 295 GGAGATG -> AVPAPR (IN REF. 1).
FT CONFLICT 328 MQ -> IE (IN REF. 1).
SQ SEQUENCE 547 AA; 56709 MW; 24E15CCC9A590CB4 CRC64;

Query Match 33.8%; Score 115.5; DB 1; Length 547;
Best Local Similarity 37.5%; Pred. No. 0.00061;
Matches 27; Conservative 14; Mismatches 26; Indels 5; Gaps 1;

QY 3 EIPAPLAGTYSK-----ILVKEGDTYKAGOTVLEAMKMETEINAPTDGKVEKVLVKER 57
DB 121 DKVPDPSAGKAVIEWVMVWYKAGDTVEADQSLTLESDKASMEIPSPAGVSVSIKVG 180
QY 58 DAVGGGGLIKI 69
DB 181 DEVTGDLILKL 192

RESULT 26
ID BTB7 MYCTU STANDARD; PRT; 70 AA.
AC 005845;
DT 18-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE Biotinylated protein TB7.3.
GN RV221C OR MT3317 OR MTCY07D11.05 OR MB3247C.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
CX NCBI_TaxID=1773, 1765;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigemeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

-----
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
[2]
SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Winn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains.";
RL J. Bacteriol. 184:5479-5490(2002).
RN [3]
SEQUENCE OF 1-15, AND BIOTINYLATION.
RC SPECIES=M.tuberculosis;
RX MEDLINE=20072687; PubMed=10603390;
RA Skjot R.L., Oettinger T., Rosenkrands I., Ravn P., Brock I.,
RA Jacobsen S., Andersen P.;
RT "Comparative evaluation of low-molecular-mass proteins from
Mycobacterium tuberculosis identifies members of the ESAT-6 family as
immunodominant T-cell antigens.";
RL Infect. Immun. 68:214-220(2000).
RN [4]
SEQUENCE FROM N.A.
RC SPECIES=M.bovis; STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972;
RA Garnier T., Eigemeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).

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EMBL; Z95120; CAB08316.1; -
EMBL; AB007143; AAK47659.1; ALT_INIT.
EMBL; BX248345; CAD93339.1; -
PIR; F70596; F70596.
HSSP; P10802; 11YU.
TIGR; MT3317; -
TubercuList; RV3221C; -
InterPro; IPR001882; Biotin_BS.
InterPro; IPR000089; Biotin_lipoyl.
Pfam; PF00364; biotin_lipoyl; 1.
PROSITE; PS00188; BIOTIN; FALSE NEG.
KW Biotin; Antigen; Complete proteome.
FT INIT_MET 0
FT BINDING 36 0 BIOTIN (BY SIMILARITY).
SQ SEQUENCE 70 AA; 7175 MW; 08B82DDD3A76892D CRC64;

Query Match 33.6%; Score 115; DB 1; Length 70;
Best Local Similarity 37.7%; Pred. No. 0.0001;
Matches 23; Conservative 13; Mismatches 25; Indels 0; Gaps 0;

QY 3 EIPAPLAGTYSKTLVKEGDTYKAGOTVLEAMKMETEINAPTDGKVEKVLVKERDAVGG 62
DB 3 DVREAIVASVLEVVVNEGQIDKGVVVLLSMEIPIVLAEGATVSKVAVSGVIVQA 62
QY 63 G 63
DB 63 G 63

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RESULT 27
ODP2 MYCCA
ID ODP2 MYCCA STANDARD; PRT; 438 AA.
AC Q49110;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase
DE complex (EC 2.3.1.12) (E2).
GN PDHC OR ODP2.
OS Mycoplasma capricolum.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2095;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=97001869; PubMed=8844861;
RA Zhu P.P., Peterkofsky A.;
RT "Sequence and organization of genes encoding enzymes involved in
RT pyruvate metabolism in Mycoplasma capricolum.";
RL Protein Sci. 5:1719-1736(1996).
CC -!- FUNCTION: THE PYRUVATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL
CC CONVERSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAINS MULTIPLE
CC COPIES OF THREE ENZYMATIC COMPONENTS: PYRUVATE DEHYDROGENASE (E1),
CC DIHYDROLIPOAMIDE ACETYLTRANSFERASE (E2) & LIPOAMIDE DEHYDROGENASE
CC (E3) (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
CC acetyldihydrolipoamide.
CC -!- COFACTOR: Contains 1 covalently bound lipoyl cofactor (By
CC similarity).
CC -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral
CC symmetry (By similarity).
CC -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC -!- SIMILARITY: Contains 1 lipoyl-binding domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U62057; AAC44344.1; -
DR HSSP; P07016; 1C4T.
DR InterPro; IPR001078; 2Oxoacid dh.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR004167; E3 binding.
DR InterPro; IPR003016; Lipoyl BS.
DR Pfam; PF00198; 2-oxoacid dh; 1.
DR Pfam; PF00364; biotin lipoyl; 1.
DR Pfam; PF02817; e3 binding; 1.
DR ProDom; PD00115; 2Oxoacid dh; 1.
DR PROSITE; PS00189; LIPOYL; 1.
KW Glycolysis; Transference; Acyltransferase; Lipoyl.
FT BINDING 42 42 LIPOYL (BY SIMILARITY).
FT ACT SITE 411 411 POTENTIAL.
SQ SEQUENCE 438 AA; 46927 MW; 4BF93B697480B4B CRC64;

Query Match 33.3%; Score 114; DB 1; Length 438;
Best Local Similarity 38.3%; Pred. No. 0.00069;
Matches 23; Conservative 16; Mismatches 21; Indels 0; Gaps 0;

QY 10 GTVSKILVKGEDVTKAGOTVILVLEMKMETEINAPTDGKVKVLVKERDAVQGGGLIKI 69
Db 16 GTVAELVKVGDVVKVQSGSLYFVETDKVNSEIPAPVAGKIATINIKAGQEIKNVGVNMEI 75

RESULT 28
ODP2_ECOLI
ID ODP2_ECOLI STANDARD; PRT; 629 AA.
AC P06959;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)

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DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase
DE complex (EC 2.3.1.12) (E2).
GN ACEF OR B0115.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
SEQUENCE FROM N.A.
RX STRAIN=K12;
RX MEDLINE=83234434; PubMed=6345153;
RA Stephens P.E., Darlison M.G., Lewis H.M., Guest J.R.;
RT "The pyruvate dehydrogenase complex of Escherichia coli K12.
RT Nucleotide sequence encoding the dihydrolipoamide acetyltransferase
RT component.";
RL Eur. J. Biochem. 133:481-489(1983).
RN [2]
SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
SEQUENCE OF 1-12.
RX STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313(1997).
RN [4]
SEQUENCE OF 34-46.
RX MEDLINE=84256520; PubMed=6821375;
RA Hale G., Perham R.N.;
RT "Amino acid sequence around lipoic acid residues in the pyruvate
RT dehydrogenase multienzyme complex of Escherichia coli.";
RL Biochem. J. 187:905-908(1980).
RN [5]
MUTAGENESIS OF HIS-602.
RX MEDLINE=90351365; PubMed=2201286;
RA Russel G.C., Guest J.R.;
RT "Overexpression of restructured pyruvate dehydrogenase complexes and
RT site-directed mutagenesis of a potential active-site histidine
RT residue.";
RL Biochem. J. 269:443-450(1990).
RN [6]
LIPOYLATED DOMAINS STUDIES.
RX MEDLINE=91024917; PubMed=2121129;
RA Ali S.T., Guest J.R.;
RT "Isolation and characterization of lipoylated and unlipoylated
RT domains of the E2p subunit of the pyruvate dehydrogenase complex of
RT Escherichia coli.";
RL Biochem. J. 271:139-145(1990).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC lipamide dehydrogenase (E3).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
CC acetyldihydrolipoamide.
CC -!- COFACTOR: Contains 3 covalently bound lipoyl cofactors.
CC -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral
CC symmetry.
CC -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC -!- SIMILARITY: Contains 3 lipoyl-binding domains.
CC
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EMBL; V01498; CAA24741.1; --  
EMBL; D26562; BAB96685.1; --  
EMBL; AE000120; AAC73226.1; --  
PIR; A30278; XXECDP.  
PDB; 1QJ0; 21-JUL-00.  
SWISS-2DPAGE; P06959; COLI.  
EC02DBASE; C062.7; 6TH EDITION.  
EC02DBASE; C062.0; 6TH EDITION.  
EcGene; EGI0025; aceF.  
InterPro; IPR001078; 2Oxoacid dh.  
InterPro; IPR006256; AceF.  
InterPro; IPR000089; Biotin lipoyl.  
InterPro; IPR004167; E3 binding.  
InterPro; IPR003016; Lipoyl\_BS.  
Pfam; PF00199; 2-oxoacid dh; 1.  
Pfam; PF00364; biotin lipoyl; 3.  
Pfam; PF02817; e3 binding; 1.  
ProDom; PD001115; 2Oxoacid dh; 1.  
TIGRfams; TIGR01348; PDHac-trf\_long; 1.  
PROSITE; PS00189; LIPOYL; 3.  
Glycolysis; Transferrase; Acyltransferase; Repeat; Lipoyl;  
Complete proteome; 3D-structure.  
INIT MET 0 0  
DOMAIN 1 314 LIPOYL BINDING, ACIDIC.  
DOMAIN 316 629 SUBUNIT BINDING, CATALYTIC.  
DOMAIN 372 388 HYDROPHOBIC.  
DOMAIN 541 566 HYDROPHOBIC.  
BINDING 40 40 LIPOYL.  
BINDING 143 143 LIPOYL.  
BINDING 244 244 LIPOYL.  
ACT\_SITE 546 546 POTENTIAL.  
ACT\_SITE 602 602 POTENTIAL.  
ACT\_SITE 606 606 POTENTIAL.  
REPEAT 1 102 REPEAT.  
REPEAT 103 203 REPEAT.  
REPEAT 204 313 REPEAT.  
MUTAGEN 602 602 H->C; ABOLISHES CATALYTIC ACTIVITY.  
SEQUENCE 629 AA; 65964 MW; 058751268B2CCCCO CRC64;  
Query Match 33.2%; Score 113.5; DB 1; Length 629;  
Best Local Similarity 34.0%; Pred. No. 0.0011;  
Matches 32; Conservative 9; Mismatches 26; Indels 27; Gaps 3;  
QY 3 EIPAPLAGTGVSKILVKEGDTVKAGQTVLVE-----AMKMET----- 39  
DB 147 EVPAFFAGTGVKEIKVNVGDKYSTGSLINWVFVAGEAGAAAPAKQEAAPAAAPAPAGVK 206  
QY 40 EINAPTDG----KVEKVLVKERDAVQGGGLIKI 69  
DB 207 EVNVPDVGDEVEVTEVNVKVGDKVAAEQSLITV 240  
RESULT 29  
PCCA RAT  
ID\_PCCA RAT STANDARD; PRT; 704 AA.  
AC P14882;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Propionyl-CoA carboxylase alpha chain, mitochondrial precursor  
DE (EC 6.4.1.3) (PCCase alpha subunit) (Propanoyl-CoA:carbon dioxide  
DE ligase alpha subunit) (Fragment).  
GN PCCA.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;

SEQUENCE FROM N.A.  
MEDLINE-89308706; PubMed-2745462;  
Browner M.F., Taroni F., Stul E., Rosenberg L.E.;  
"sequence analysis, biogenesis, and mitochondrial import of the  
alpha-subunit of rat liver propionyl-CoA carboxylase.";  
J. Biol. Chem. 264:12680-12685(1989).  
[2]  
REVIEWS.  
Browner M.F., Taroni F., Stul E., Rosenberg L.E.;  
Submitted (FEB-1989) to the EMBL/GenBank/DBJ databases.  
CC -! CATALYTIC ACTIVITY: ATP + propanoyl-CoA + HCO(3) (-) = ADP +  
CC phosphate + (S)-methylmalonyl-CoA.  
CC -! COFACTOR: Biotin.  
CC -! PATHWAY: Key enzyme in the catabolic pathway of odd-chain fatty  
CC acids, isoleucine, threonine, methionine, and valine.  
CC -! SUBUNIT: Probably a dodecamer composed of six biotin-containing  
CC alpha subunits and six beta subunits.  
CC -! SUBCELLULAR LOCATION: Mitochondrial matrix.  
CC -! DISEASE: Propionic acidemia due to recessively inherited  
CC deficiency of PCCase activity often causes life-threatening  
CC ketosis and acidosis.  
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EMBL; M22631; AAA88512.1; ALT\_SEQ.  
HSSP; P24182; 1DVI.  
InterPro; IPR001882; Biotin BS.  
InterPro; IPR005482; Biotin\_Carb C.  
InterPro; IPR000089; Biotin\_lipoyl.  
InterPro; IPR005479; CPhase\_L D2.  
InterPro; IPR005481; CPhase\_L N.  
Pfam; PF02785; Biotin carb C; 1.  
Pfam; PF00364; biotin lipoyl; 1.  
Pfam; PF00289; CPhase\_L chain; 1.  
Pfam; PF02786; CPhase\_L D2; 1.  
PROSITE; PS00188; BIOTIN; 1.  
PROSITE; PS00866; CPSASE\_1; 1.  
PROSITE; PS00867; CPSASE\_2; 1.  
Mitochondrion; Ligase; Biotin; ATP-binding; Transit peptide.  
NON\_TER 1 1  
TRANSIT <1 21 MITOCHONDRION.  
CHAIN 22 704 PROPIONYL-CoA CARBOXYLASE ALPHA CHAIN.  
NP\_BIND 199 204 ATP (POTENTIAL).  
ACT\_SITE 329 329 BY SIMILARITY.  
BINDING 670 670 BIOTIN (BY SIMILARITY).  
SEQUENCE 704 AA; 77711 MW; 36CEC52DF2D2A8A CRC64;  
Query Match 32.5%; Score 111; DB 1; Length 704;  
Best Local Similarity 40.6%; Pred. No. 0.0021;  
Matches 26; Conservative 10; Mismatches 28; Indels 0; Gaps 0;  
QY 6 APLAGTGVSKILVKEGDTVKAGQTVLVEAMKMETEINAPTDGKVKVLVKERDAVQGGG 65  
DB 640 SPKEGVVAVSVKPGDMVAEGQECVTEAMKQNSMTAGKMGKVLVHCKAGDTVGSGDL 699  
QY 66 LIKI 69  
DB 700 LEVEL 703  
RESULT 30  
PCCA HUMAN  
ID\_PCCA HUMAN STANDARD; PRT; 703 AA.  
AC P05165; Q15979;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)



DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Propionyl-CoA carboxylase alpha chain, mitochondrial precursor  
 DE (EC 6.4.1.3) (PCCase alpha subunit) (Propionyl-CoA:carbon dioxide  
 DE ligase alpha subunit).  
 GN PCCA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=89296507; PubMed=2740237;  
 RA Lamhonwah A.-M., Mahuran D.J., Gravel R.A.;  
 RT "Human mitochondrial propionyl-CoA carboxylase: localization of the  
 RT N-terminus of the pro- and mature alpha chains in the deduced  
 RT primary sequence of a full-length cDNA.";  
 RL Nucleic Acids Res. 17:4396-4396(1989).  
 RN [2]  
 RP REVISIONS.  
 RA Gravel R.A.;  
 RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Campeau E., Desviat L.R., Leclerc D., Perez B., Ugarte M.,  
 RA Gravel R.A.;  
 RT "Structure of the PCCA gene and distribution of mutations in propionic  
 RT acidemia.";  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buetow K.H., Sherman C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldi M.F., Cagavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshitsuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McWeeney P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16901(2002).  
 RN [5]  
 RP SEQUENCE OF 344-536 FROM N.A.  
 RX MEDLINE=86259695; PubMed=3460076;  
 RA Lamhonwah A.-M., Barankiewicz T.J., Willard H.F., Mahuran D.J.,  
 RA Quan F., Gravel R.A.;  
 RT "Isolation of cDNA clones coding for the alpha and beta chains of  
 RT human propionyl-CoA carboxylase: chromosomal assignments and DNA  
 RT polymorphisms associated with PCCA and PCCB genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:4864-4868(1986).  
 RN [6]  
 RP SEQUENCE OF 339-367 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=93167265; PubMed=8434582;  
 RA Stankovics J., Ledley F.D.;  
 RT "Cloning of functional alpha propionyl CoA carboxylase and correction  
 RT of enzyme deficiency in pcca fibroblasts.";  
 RL Am. J. Hum. Genet. 52:144-151(1993).  
 RN [7]  
 RP SEQUENCE OF 608-703 FROM N.A.  
 RX MEDLINE=87212051; PubMed=3555348;  
 RA Lamhonwah A.-M., Quan F., Gravel R.A.;

"Sequence homology around the biotin-binding site of human  
 propionyl-CoA carboxylase and pyruvate carboxylase.";  
 Arch. Biochem. Biophys. 254:631-636(1987).  
 RN [8]  
 RP REVIEW ON PA VARIANTS.  
 RX MEDLINE=99433966; PubMed=10502773;  
 RA Ugarte M., Perez-Cerda C., Rodriguez-Pombo P., Desviat L.R., Perez B.,  
 RA Richard E., Muro S., Campeau E., Ohura T., Gravel R.A.;  
 RT "Overview of mutations in the PCCA and PCCB genes causing propionic  
 RT acidemia.";  
 RL Hum. Mutat. 14:275-282(1999).  
 RN [9]  
 RP VARIANTS PA-1 THR-52; THR-113; THR-139; LYS-348 AND ARG-606.  
 RX MEDLINE=92203168; PubMed=10101253;  
 RA Richard E., Desviat L.R., Perez B., Perez-Cerda C., Ugarte M.;  
 RT "Genetic heterogeneity in propionic acidemia patients with alpha-  
 RT subunit defects: identification of five novel mutations, one of them  
 RT causing instability of the protein.";  
 RL Biochim. Biophys. Acta 1453:351-358(1999).  
 RN [10]  
 RP VARIANTS PA-1 PRO-50; LYS-204; GLY-343; VAL-354; ARG-643 AND CYS-687  
 RP DEL.  
 RX MEDLINE=99263311; PubMed=10329019;  
 RA Campeau E., Dupuis L., Leon-Del-Rio A., Gravel R.;  
 RT "Coding sequence mutations in the alpha subunit of propionyl-CoA  
 RT carboxylase in patients with propionic acidemia.";  
 RL Mol. Genet. Metab. 67:11-22(1999).  
 CC -! CATALYTIC ACTIVITY: ATP + propionyl-CoA + HCO(3) (-) = ADP +  
 CC phosphate + (S)-methylmalonyl-CoA.  
 CC -! COFACTOR: Biotin.  
 CC -! PATHWAY: Key enzyme in the catabolic pathway of odd-chain fatty  
 CC acids, isoleucine, threonine, methionine, and valine.  
 CC -! SUBUNIT: Probably a dodecamer composed of six biotin-containing  
 CC alpha subunits and six beta subunits.  
 CC -! SUBCELLULAR LOCATION: Mitochondrial matrix.  
 CC -! DISEASE: Defects in PCCA are the cause of propionic acidemia type  
 CC I (PA-1) (MIM:606054). PA-1 is a life-threatening disease  
 CC characterized by episodic vomiting, lethargy and ketosis,  
 CC neutropenia, periodic thrombocytopenia, hypogammaglobulinemia,  
 CC developmental retardation, and intolerance to protein.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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 EMBL; X14608; CAA32763.1; -  
 EMBL; AY035808; AAK61392.1; -  
 EMBL; AY035786; AAK61392.1; JOINED.  
 EMBL; AY035787; AAK61392.1; JOINED.  
 EMBL; AY035788; AAK61392.1; JOINED.  
 EMBL; AY035789; AAK61392.1; JOINED.  
 EMBL; AY035790; AAK61392.1; JOINED.  
 EMBL; AY035791; AAK61392.1; JOINED.  
 EMBL; AY035792; AAK61392.1; JOINED.  
 EMBL; AY035793; AAK61392.1; JOINED.  
 EMBL; AY035794; AAK61392.1; JOINED.  
 EMBL; AY035795; AAK61392.1; JOINED.  
 EMBL; AY035796; AAK61392.1; JOINED.  
 EMBL; AY035797; AAK61392.1; JOINED.  
 EMBL; AY035798; AAK61392.1; JOINED.  
 EMBL; AY035799; AAK61392.1; JOINED.  
 EMBL; AY035800; AAK61392.1; JOINED.  
 EMBL; AY035801; AAK61392.1; JOINED.  
 EMBL; AY035802; AAK61392.1; JOINED.  
 EMBL; AY035803; AAK61392.1; JOINED.  
 EMBL; AY035804; AAK61392.1; JOINED.  
 EMBL; AY035805; AAK61392.1; JOINED.  
 EMBL; AY035806; AAK61392.1; JOINED.  
 EMBL; AY035807; AAK61392.1; JOINED.

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DR EMBL; BC000140; AAH00140.1; -.
DR DR EMBL; M13572; AAA60035.1; -.
DR DR EMBL; S55656; AAB25345.1; -.
DR DR EMBL; M26121; AAA36424.1; -.
DR DR PIR; S04613; A27883.
DR DR HSP; P24182; IDVL.
DR DR Genew; HGNC:8653; PCCA.
DR DR MIM; 232000; -.
DR DR MIM; 606054; -.
DR DR GO; GO:0009374; F:biotin binding; TAS.
DR DR GO; GO:0004658; F:propionyl-CoA carboxylase activity; TAS.
DR DR InterPro; IPR001882; Biotin_BS.
DR DR InterPro; IPR005482; Biotin_carb_C.
DR DR InterPro; IPR000089; Biotin_lipoyl.
DR DR InterPro; IPR005479; CPase_L_D2.
DR DR InterPro; IPR005481; CPase_L_N.
DR DR Pfam; PF02785; Biotin_carb_C; 1.
DR DR Pfam; PF00364; Biotin_lipoyl; 1.
DR DR Pfam; PF02829; CPase_L_D2; 1.
DR DR Pfam; PF02786; CPase_L_D2; 1.
DR DR PROSITE; PS00188; BIOTIN; 1.
DR DR PROSITE; PS00866; CPASE; 1.
DR DR PROSITE; PS00867; CPASE2; 1.
DR DR Mitochondrion; Ligase; Biotin; ATP-binding; Transit peptide;
KW Disease mutation; Polymorphism.
KW TRANSIT 1 20 MITOCHONDRION.
FT CHAIN 21 703 PROPIONYL-COA CARBOXYLASE ALPHA CHAIN.
FT NP_BIND 198 203 ATP (POTENTIAL).
FT ACT_SITE 328 328 BY SIMILARITY.
FT BINDING 669 669 BIOTIN (BY SIMILARITY).
FT VARIANT 50 50 A -> P (in PA-1).
FT VARIANT 52 52 /FTID=VAR.009087.
FT VARIANT 113 113 R -> W (in PA-1).
FT VARIANT 139 139 A -> T (in PA-1).
FT VARIANT 204 204 I -> T (in PA-1).
FT VARIANT 272 272 M -> K (in PA-1).
FT VARIANT 343 343 Q -> R (in PA-1).
FT VARIANT 348 348 D -> G (in PA-1).
FT VARIANT 354 354 M -> K (in PA-1; unstable protein).
FT VARIANT 374 374 G -> V (in PA-1).
FT VARIANT 374 374 R -> Q (in PA-1).
Query Match 32.24; Score 110; DB 1; Length 703;
Best Local Similarity 37.54; Pred. No. 0.0026;
Matches 24; Conservative 12; Mismatches 28; Indels 0; Gaps 0;
QY 6 APLAGTYSKILVKEGDTVKAGOTVLVLEAMKMETEINAPDGVKVKLVKERAQVQGGQ 65
Db 639 SMPGVVAVSVKGDVAEGQIEICVTEAMKQNSMTAGTGTGVKSVHCQAGDTVGEGDL 698
QY 66 LIKI 69
Db 699 LVEL 702
RESULT 31
BCCP CHLPN
ID ~BCCP CHLPN STANDARD; PRT; 167 AA.
AC Q92901; 2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP).
GN ACCEB OR CFN0183 OR CP0585 OR CPB0186.

```

OS Chlamydia pneumoniae (Chlamydia pneumoniae).  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=83558;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CWL029;  
RX MEDLINE=99206606; PubMed=10192388;  
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,  
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;  
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis";  
RL Nat. Genet. 21:385-389(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AR39;  
RX MEDLINE=20150255; PubMed=10684935;  
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,  
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,  
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,  
RA Eisen J., Fraser C.M.;  
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia  
RL pneumoniae AR39";  
RN Nucleic Acids Res. 28:1397-1406(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=J138;  
RX MEDLINE=20330349; PubMed=10871362;  
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,  
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;  
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138  
RL from Japan and CWL029 from USA";  
RN Nucleic Acids Res. 28:2311-2314(2000).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TW-183;  
RA Geng M.M., Schumacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,  
RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;  
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with  
RL other Chlamydia strains based on whole genome sequence analysis";  
CC Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: This protein is a component of the acetyl coenzyme A  
CC carboxylase complex; first, biotin carboxylase catalyzes the  
CC carboxylation of the carrier protein and then the transcarboxylase  
CC transfers the carboxyl group to form malonyl-CoA (by similarity).  
CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.  
CC -!- SUBUNIT: Homodimer (By similarity).  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AE001604; AAD18336.1; -  
CC EMBL; AE002217; AAF38403.1; -  
CC EMBL; AP002545; BAA98393.1; -  
CC EMBL; AE017157; BAA98119.1; -  
CC PIR; F72110; F72110.  
CC PIR; G86513; G86513.  
CC HSSP; P02905; 3BDO.  
CC PHCI-2DPAGE; Q32901; -  
CC TIGR; CP0585; -  
CC InterPro; IPR001249; AccCoA\_biotinCC.  
CC InterPro; IPR001882; Biotin\_BS.  
CC InterPro; IPR000089; Biotin\_lipoyl.  
CC Pfam; PF00364; biotin\_lipoyl; 1.  
CC PRINTS; PR01071; AC0AEI0INC.  
CC TIGRFAMS; TIGR00531; BCCP; 1.  
CC PROSITE; PS00188; BIOTIN; 1.  
KW Fatty acid biosynthesis; Biotin; Complete proteome.  
FT BINDING 129 129 BIOTIN (BY SIMILARITY).

```

SQ SEQUENCE 167 AA; 18461 MW; AAA1CF1801F9CE4C CRC64;
Query Match 31.7%; Score 108.5; DB 1; Length 167;
Best Local Similarity 38.4%; Pred. No. 0.00095;
Matches 28; Conservative 9; Mismatches 29; Indels 7; Gaps 1;
QY 4 IPAPLAGTV-----SKILVKGDTVKAGQTVLVLEAMKMETEINAPTQKGVKVLVKE 56
Db 90 ISSFLVGTFFYSGPAPDSFVKPGDIVSEDTIVCIIVKMKVNEVKAGMSRVLEVLITN 149
QY 57 RDVAVGGGQGLIKI 69
Db 150 GDPVQFGSKLFRI 162

RESULT 32
ODO2 MYCTU STANDARD; PRT; 553 AA.
AC Q10381;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Dihydrolipoamide succinyltransferase component of 2-oxoglutarate
DE dehydrogenase complex [EC 2.3.1.61] (E2).
GN SUCB OR RV2215 OR MT2272 OR MTCY190.26 OR MB2238.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37Rv;
RX MEDLINE=98293987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=2206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL J. Bacteriol. 184:5479-5490(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.bovis; STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972;
RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrett B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
CC -!- FUNCTION: THE 2-OXOGLUTARATE DEHYDROGENASE COMPLEX CATALYZES THE
CC OVERALL CONVERSION OF 2-OXOGLUTARATE TO SUCCINYL-CoA & CO(2). IT
CC CONTAINS MULTIPLE COPIES OF 3 ENZYMIC COMPONENTS: 2-OXOGLUTARATE
CC DEHYDROGENASE (E1), DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE (E2) AND
CC LIPOAMIDE DEHYDROGENASE (E3) [BY SIMILARITY].
CC -!- CATALYTIC ACTIVITY: Succinyl-CoA + dihydrolipoamide = CoA + S-
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CC succinyl-dihydrolipoamide.
CC -!- COFACTOR: Contains 2 covalently bound lipoyl cofactors
CC (Potential).
CC -!- PATHWAY: Tricarboxylic acid cycle.
CC -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral
CC symmetry (By similarity).
CC -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.
CC -----
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CC -----
CC EMBL; Z70283; CAA94256.1; -.
CC EMBL; AE007072; AAK46557.1; -.
CC EMBL; BX248341; CAD97091.1; -.
CC PIR; H70786; H70786.
CC HSP; P07016; 1C4T.
CC TIGR; MT2272; -.
CC TubercuList; RV2215; -.
CC InterPro; IPR001078; 2Oxoacid dh.
CC InterPro; IPR000089; Biotin lipoyl.
CC InterPro; IPR004167; E3 binding.
CC InterPro; IPR003016; Lipoyl_P8.
CC Pfam; PF00198; 2-oxoacid dh; 1.
CC Pfam; PF00364; biotin lipoyl; 2.
CC Pfam; PF02817; e3 binding; 1.
CC ProDom; PD001115; 2Oxoacid dh; 1.
CC PROSITE; PS00189; Lipoyl; 2.
CC Tricarboxylic acid cycle; Transferase; Acyltransferase; Lipoyl;
KW Complete proteome.
FT BINDING 43 43 LIPOYL (POTENTIAL).
FT BINDING 162 162 LIPOYL (POTENTIAL).
FT ACT_SITE 523 523 BY SIMILARITY.
FT ACT_SITE 527 527 BY SIMILARITY.
SQ SEQUENCE 553 AA; 57087 MW; 5486E70D23B804A7 CRC64;

Query Match 31.6%; Score 108; DB 1; Length 553;
Best Local Similarity 37.7%; Pred. No. 0.0033;
Matches 23; Conservative 16; Mismatches 22; Indels 0; Gaps 0;
QY 10 GTVSKILVKGDTVKAGQTVLVLEAMKMETEINAPTQKGVKVLVKEADVQGGGLIKI 69
Db 17 GTVTRWLKQEGDTVELDEPLVEVSTDKVDTETPSAAGVLTKITAQEDDTVEVGGLAVI 76
QY 70 G 70
Db 77 G 77

RESULT 33
BTB7 MYCLE STANDARD; PRT; 70 AA.
AC Q9CCH9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Biotinylated protein TB7.3 homolog.
GN ML0802.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TN.
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
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RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC
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CC
CC EMBL; AL583919; CAC30312.1; ALT_INIT.
CC HSPF; P10802; ILYU.
CC Leprona; M10802; -.
CC InterPro; IPR001882; Biotin BS.
CC InterPro; IPR000089; Biotin_lipoyl.
CC Pfam; PF00364; biotin_lipoyl; 1.
CC PROSITE; PS00188; BIOTIN; FALSE_NEG.
KW Biotin; Complete proteome.
FT INIT MET 0 0 BY SIMILARITY.
FT BINDING 36 36 BIOTIN (BY SIMILARITY).
SQ SEQUENCE 70 AA; 7088 MW; B519F389DEF0447D CRC64;

Query Match 31.3%; Score 107; DB 1; Length 70;
Best Local Similarity 36.1%; Pred. No. 0.0059;
Matches 22; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

Oy 3 EIPAPLAGTSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKLVKRDVAVQG 62
Db 3 DVRAEIVASVLEVVVSEGDQIGKGDVLVLESMEKWEIPVLGAVIGSVSVSGDVIIQA 62

Oy 63 G 63
Db 63 G 63

RESULT 34
DURI YEAST STANDARD; PRT; 1835 AA.
AC P32528;
AD 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Urea amidolyase [includes: Urea carboxylase (EC 6.3.4.6); Allophanate
DE hydrolase (EC 3.5.1.54)].
GN DURI,2 OR YBR208C OR YBR1448.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_taxid=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92199240; PubMed=1802034;
RA Genbauffe F.S., Cooper T.G.;
RT "The urea amidolyase (DURI,2) gene of Saccharomyces cerevisiae.";
RL DNA Seq. 2:119-32(1991).
RN [2]
RP SEQUENCE OF 1-893 FROM N.A.
RC STRAIN=S288c;
RA Rieger M.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 873-1835 FROM N.A.
RC STRAIN=S288c;
RA Feldmann H., Mannhaupt G., Schwarzlose C., Vetter I.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.

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RN [4]
RP SEQUENCE OF 1487-1835 FROM N.A.
RC STRAIN=S288c;
RX MEDLINE=93377417; PubMed=8368014;
RA Bussereau F., Mallet L., Gaillon L., Jacquet M.;
RT "A 12.8 kb segment, on the right arm of chromosome II from
RT Saccharomyces cerevisiae, including part of the DURI,2 gene, contains
RT five putative new genes.";
RL Yeast 9:797-806(1993).
CC
CC -1- FUNCTION: Hydrolysis of urea to ammonia and CO2.
CC -1- CATALYTIC ACTIVITY: ATP + urea + CO(2) = ADP + phosphate + urea-1-
CC carboxylate.
CC -1- CATALYTIC ACTIVITY: Urea-1-carboxylate + H(2)O = 2 CO(2) + 2
CC NH(3).
CC -1- COFACTOR: Biotin.
CC -1- PATHWAY: Allantoin and arginine metabolism.
CC -1- SUBUNIT: Monomer.
CC -1- INDUCTION: By allophanate or its non-metabolized analog
CC oxalurate. Repressed in the presence of readily used nitrogen
CC sources.
CC
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CC
CC EMBL; M64926; AAC41643.1; -.
CC EMBL; Z36077; CAA85172.1; -.
CC EMBL; Z21487; CAA79695.1; -.
CC PIR; S46082; S46082.
CC HSPF; P24182; IBNC.
CC GerMOnline; 138751; -.
CC SGD; S0000412; DURI,2.
CC GO; GO:0004039; F:allophanate hydrolase activity; IMP.
CC GO; GO:0004847; F:urea carboxylase activity; IMP.
CC GO; GO:0019627; P:urea metabolism; IMP.
CC InterPro; IPR000120; Amidase.
CC InterPro; IPR001882; Biotin BS.
CC InterPro; IPR005482; Biotin carb C.
CC InterPro; IPR000089; Biotin_lipoyl.
CC InterPro; IPR005479; CPase_L_D2.
CC InterPro; IPR005481; CPase_L_N.
CC InterPro; IPR003778; DUF183.
CC InterPro; IPR003833; DUF213.
CC Pfam; PF02682; AHS1; 1.
CC Pfam; PF02626; AHS2; 1.
CC Pfam; PF01425; Amidase; 1.
CC Pfam; PF02785; Biotin carb C; 1.
CC Pfam; PF00364; biotin_lipoyl; 1.
CC Pfam; PF00289; CPase_L_chain; 1.
CC Pfam; PF02786; CPase_L_D2; 1.
CC PROSITE; PS00188; BIOTIN; 1.
CC PROSITE; PS00866; CPASE_1; 1.
CC PROSITE; PS00867; CPASE_2; 1.
KW Ligase; Hydrolase; Multifunctional enzyme; Arginine metabolism;
KW Biotin; ATP-binding.
FT NP BIND 122 129 ATP (POTENTIAL).
FT BINDING 1798 1798 BIOTIN.
FT CONFLICT 96 96 P -> R (IN REF. 1).
FT CONFLICT 256 258 LKK -> KKN (IN REF. 1).
FT CONFLICT 459 459 I -> M (IN REF. 1).
FT CONFLICT 830 830 E -> K (IN REF. 1).
FT CONFLICT 1395 1395 D -> E (IN REF. 1).
SQ SEQUENCE 1835 AA; 201831 MW; F52BDDDOFE42CD65 CRC64;

Query Match 30.4%; Score 104; DB 1; Length 1835;
Best Local Similarity 40.0%; Pred. No. 0.024;
Matches 22; Conservative 10; Mismatches 23; Indels 0; Gaps 0;

Oy 9 AGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKLVKRDVAVQG 63

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Db 1771 SGRFWKSIASVDVIEACQGLLIIEAMKAEMLIISAPKSGKIICKICHGNDWDSG 1825

RESULT 35

ODP2\_HAEIN STANDARD; PRT; 567 AA.

AC P45118;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) (E2).

GN ACEF OR H1232.

OS Haemophilus influenzae.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

OC Pasteurellaceae; Haemophilus.

OC NCBI\_TaxID=727;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=rd / KW20 / ATCC 51907;

RA MEDLINE=95350630; PubMed=7542800;

RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;

RT "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";

RL Science 269:496-512(1995).

CC -!- FUNCTION: THE PYRUVATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL CONVERSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAINS MULTIPLE COPIES OF THREE ENZYMOLOGIC COMPONENTS: PYRUVATE DEHYDROGENASE (E1), DIHYDROLIPOAMIDE ACETYLTRANSFERASE (E2) & LIPOAMIDE DEHYDROGENASE (E3) (BY SIMILARITY).

CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-acetyldihydrolipoamide.

CC -!- COFACTOR: Contains 2 covalently bound lipoyl cofactors (By similarity).

CC -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral symmetry (By similarity).

CC -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.

CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.

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DR EMBL; U32803; AAC22885.1; -.

DR F164111; I64111.

DR HSP; F10802; 1DFC.

DR TIGR; H11232; -.

DR InterPro; IPR001078; 2Oxoacid\_dh.

DR InterPro; IPR006256; AceF.

DR InterPro; IPR000089; Biotin\_lipoyl.

DR InterPro; IPR004167; E3\_binding.

DR Pfam; PF001198; 2-oxoacid\_dh; 1.

DR Pfam; PF00364; biotin\_lipoyl; 2.

DR Pfam; PF02817; e3\_binding; 1.

DR ProDom; PD001115; 2Oxoacid\_dh; 1.

DR TIGRFAMs; TIGR01348; PDHac\_trf\_long; 1.

DR PROSITE; PS00189; LIPOYL; 2.

KW Glycolysis; Transferase; Acyltransferase; Repeat; Lipoyl; Complete proteome.

FT DOMAIN 1 245 LIPOYL BINDING, ACIDIC.

FT DOMAIN 247 567 SUBUNIT BINDING, CATALYTIC.

FT BINDING 41 41 LIPOYL (BY SIMILARITY).

FT BINDING 147 147 LIPOYL (BY SIMILARITY).

FT ACT\_SITE 484 484 POTENTIAL.

FT ACT\_SITE 540 540 POTENTIAL.

FT ACT\_SITE 544 544 POTENTIAL.

SQ SEQUENCE 567 AA; 59410 MW; 891DBCEB388C5B0 CRC64;

Query Match 30.3%; Score 103.5; DB 1; Length 567;

Best Local Similarity 23.7%; Pred. No. 0.009;

Matches 32; Conservative 10; Mismatches 24; Indels 69; Gaps 1;

QY 3 EIPAPLAGTVSKILVKGSDTVKAGQTVLVLEAM----- 35

Db 45 EVPAPEAGVWKEILLVKVGKSTGTGTPMLVLEAAGAAPADEPTAPVADAPTPVAVTAPT 104

QY 36 -----KMETEINAPTQKVKVXL 53

Db 105 ASAIVEVNVDPDGGDEVNVTIMVAVGDTITEQSLITVEGDKASMEVPAEPFGVWKEIL 164

QY 54 VKERDAVGGGGLIK 68

Db 165 VKSGDKVSTGSLIMR 179

RESULT 36

ODP2\_ZYMO STANDARD; PRT; 462 AA.

ID ODP2\_ZYMO

AC O66113; O69012;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Pyruvate dehydrogenase E1 component, beta subunit (EC 1.2.4.1).

GN PDH OR PDHABETA.

OS Zymomonas mobilis.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;

OC Sphingomonadaceae; Zymomonas.

ON NCBI\_TaxID=542;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 29191 / ZM6;

RA MEDLINE=98175679; PubMed=9515924;

RA Neveling U., Klaseen R., Bringer-Meyer S., Sahm H.;

RT "Purification of the pyruvate dehydrogenase multienzyme complex of Zymomonas mobilis and identification and sequence analysis of the corresponding genes.";

RT J. Bacteriol. 180:1540-1548(1998).

RL [2]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 31821 / ZMA / CP4;

RA Lee J., Jin S., Kang H.S.;

RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall conversion of pyruvate to acetyl-CoA and CO(2). It contains multiple copies of three enzymatic components: pyruvate dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and lipoamide dehydrogenase (E3) (By similarity).

CC -!- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S-acetyldihydrolipoamide + CO(2).

CC -!- COFACTOR: Binds 1 thiamine pyrophosphate and 1 lipoyl cofactor per subunit.

CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.

CC -!- SIMILARITY: Contains 1 lipoyl-binding domain.

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```

DR EMBL; Y12884; CAA73385.1; -.
DR EMBL; AF086791; AAC70362.1; -.
DR HSP; P09061; IQS0.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR003016; Lipoyl_BS.
DR InterPro; IPR009014; Transketo_C_like.
DR InterPro; IPR005476; Transketolase_C.
DR InterPro; IPR005475; Transketolase_CR.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF02779; transket_pyr; 1.
DR Pfam; PF02780; transketolase_C; 1.
DR PROSITE; PS00189; LIPOYL; 1.
KW Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
KW Lipoyl.
FT BINDING 43 43 LIPOYL (POTENTIAL).
FT CONFLICT 87 87 E -> D (IN REF. 2).
FT CONFLICT 112 112 L -> V (IN REF. 2).
FT CONFLICT 232 244 SAAKTHVMGGQV -> LRPKRITCPAAKC (IN REF. 2).
FT CONFLICT 259 259 R -> P (IN REF. 2).
FT CONFLICT 262 262 A -> E (IN REF. 2).
SQ SEQUENCE 462 AA; 49860 MW; 514275F7D70C34BC CRC64;

Query Match 30.1%; Score 103; DB 1; Length 462;
Best Local Similarity 34.8%; Pred. No. 0.0083;
Matches 23; Conservative 14; Mismatches 23; Indels 6; Gaps 1;

QY 5 PAPIAGTVSKILVKGDTVKAGQTVLVLEAMKMETEINAPDVGKVKLVKVERDAVGGQ 64
DB 12 PTMBEGTLRWLVKSGSIKAGIELAETDKAIMEFAVDEGVITKILIFE-----GS 65
QY 65 GLIKIG 70
DB 66 ENVKVG 71

RESULT 37
BCCP_HAEIN
ID_BCCP_HAEIN STANDARD; PRT; 155 AA.
AC P43874;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP).
GN ACCE OR FASE OR HI0971.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shinkley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
RL Science 269:496-512 (1995).
RN [2]
RP SEQUENCE OF 1-10.
RX MEDLINE=20137488; PubMed=10675023;
RA Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
RA Gray C., Fountoulakis M.;
RT "Two-dimensional map of the proteome of Haemophilus influenzae.";
RL Electrophoresis 21:411-429 (2000).
CC -!- FUNCTION: This protein is a component of the acetyl coenzyme A

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CC carboxylase complex; first, biotin carboxylase catalyzes the
CC carboxylation of the carrier protein and then the transcarboxylase
CC transfers the carboxyl group to form malonyl-CoA (By similarity).
CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.
CC -!- SUBUNIT: Homodimer (By similarity).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U32778; AAC22631.1; -.
DR PIR; E64105; E64105.
DR HSP; P02905; IBD0.
DR TIGR; HI0971; -.
DR InterPro; IPR001249; AcCoA_biotinCC.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PRINTS; PR01071; ACOABIOFINCC.
DR TIGRFAMS; TIGR00531; BCCP; 1.
DR PROSITE; PS00189; BIOTIN; 1.
KW Fatty acid biosynthesis; Biotin; Complete proteome.
FT BINDING 121 121 BIOTIN (BY SIMILARITY).
SQ SEQUENCE 155 AA; 16247 MW; 696F19B4429A03CD CRC64;

Query Match 30.0%; Score 102.5; DB 1; Length 155;
Best Local Similarity 32.9%; Pred. No. 0.0034;
Matches 24; Conservative 16; Mismatches 26; Indels 7; Gaps 1;

QY 4 IPAPLAGTV-----SKILVKGDTVKAGQTVLVLEAMKMETEINAPTQKVEKVLVKE 56
DB 82 VRSPMVGTFYRSPSPKAFVEVQSVKVGALCTIVAMKMNRIEADKAGVKAILND 141
QY 57 RDAVGGGGGLIKI 69
DB 142 GNAVEFDEPLIV 154

RESULT 38
ODP2_ACHLA
ID_ODP2_ACHLA STANDARD; PRT; 544 AA.
AC P35489;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase
DE complex (EC 2.3.1.12) (E2).
GN PHC
OS Acholeplasma laidlawii.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Acholeplasma.
OX NCBI_TaxID=2148;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE=92138635; PubMed=1735725;
RA Wallbrant P., Tegman V., Jonsson B.-H., Wieslander A.;
RT "Identification and analysis of the genes coding for the putative
RT pyruvate dehydrogenase enzyme complex in Acholeplasma laidlawii.";
RL J. Bacteriol. 174:1388-1396 (1992).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC lipoamide dehydrogenase (E3).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
CC acetyldihydrolipoamide.
CC -!- COFACTOR: Contains 2 covalently bound lipoyl cofactors
CC (Potential).
CC -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral

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CC symmetry (By similarity).
CC -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M81753; AAA21909.1; -.
CC PIR; C42653; C42653.
CC HSSP; P07016; 1C4T.
CC InterPro; IPR001078; 2Oxoacid_dh.
CC InterPro; IPR000089; Biotin_lipoyl.
CC InterPro; IPR004167; E3_binding.
CC InterPro; IPR003016; Lipoyl_BS.
CC Pfam; PF00198; 2-oxoacid_dh; 1.
CC Pfam; PF00364; biotin_lipoyl; 2.
CC Pfam; PF02817; e3_binding; 1.
CC ProDom; PD001115; 2Oxoacid_dh; 1.
CC PROSITE; PS00189; LIPOYL; 2.
CC Glycolysis; Transferase; Acyltransferase; Lipoyl.
FT BINDING 42 42 LIPOYL (BY SIMILARITY).
FT BINDING 154 154 LIPOYL (BY SIMILARITY).
FT ACT_SITE 516 516 POTENTIAL.
SQ SEQUENCE 544 AA; 57261 MW; 81E92D869CFD5424 CRC64;

Query Match 29.8%; Score 102; DB 1; Length 544;
Best Local Similarity 35.0%; Pred. No. 0.012;
Matches 21; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 10 GTVSKILVKGDTKAGQTLVLEAMKMETEINAPTDGKVEKLVKRDVAGGGGLIKI 69
Db 16 GTVLQWNEFKVGKVEGTTLVETDKVNAELPSVDGTVSLGAKGEETIHVGQIIVTI 75

RESULT 39
ODP2_AZOV1
ID ODP2_AZOV1 STANDARD; PRT; 637 AA.
AC P10802;
DT 01-JUL-1999 (Rel. 11, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase
DE complex (EC 2.3.1.12) (E2).
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 478;
RX MEDLINE=88271330; PubMed=3292237;
RA Hanemaaijer R., Janssen A., de Kok A., Veeger C.;
RT "The dihydrolipoalyltransferase component of the pyruvate
RT dehydrogenase complex from Azotobacter vinelandii. Molecular cloning
RT and sequence analysis."
RL Eur. J. Biochem. 174:593-599(1988).
RN [2]
RP SEQUENCE OF 1-15 AND 380-415.
RX MEDLINE=88082750; PubMed=3691494;
RA Hanemaaijer R., de Kok A., Jolles J., Veeger C.;
RT "The domain structure of the dihydrolipoalyl transferase component
RT of the pyruvate dehydrogenase complex from Azotobacter vinelandii."
RL Eur. J. Biochem. 169:245-252(1987).
RN [3]
RP LIPOYL DOMAIN CONFORMATION.
RX MEDLINE=89052887; PubMed=3191993;
RA Hanemaaijer R., Vervoort J., Westphal A.H., de Kok A., Veeger C.;
RT "Mobile sequences in the pyruvate dehydrogenase complex, the E2

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RT component, the catalytic domain and the 2-oxoglutarate dehydrogenase
RT complex of Azotobacter vinelandii, as detected by 600 MHz 1H-NMR
RT spectroscopy."
RL FEBS Lett. 240:205-210(1988).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 381-637.
RX MEDLINE=92196586; PubMed=1549782;
RA Mattevi A., Obmolova G., Schulze E., Kalk K.H., Westphal A.H.,
RA de Kok A., Hol W.G.J.;
RT "Atomic structure of the cubic core of the pyruvate dehydrogenase
RT multienzyme complex."
RN Science 255:1544-1550(1992).
RN [5]
RP STRUCTURE BY NMR OF 1-78.
RX MEDLINE=94222112; PubMed=8068086;
RA Berg A., de Kok A., Vervoort J.;
RT "Sequential 1H and 15N nuclear magnetic resonance assignments and
RT secondary structure of the N-terminal lipoyl domain of the
RT dihydrolipoalyl transferase component of the pyruvate dehydrogenase
RT complex from Azotobacter vinelandii."
RL Eur. J. Biochem. 221:87-100(1994).
RN [6]
RP STRUCTURE BY NMR OF 1-78.
RX MEDLINE=97234563; PubMed=9119000;
RA Berg A., Vervoort J., de Kok A.;
RT "Three-dimensional structure in solution of the N-terminal lipoyl
RT domain of the pyruvate dehydrogenase complex from Azotobacter
RT vinelandii."
RL Eur. J. Biochem. 244:352-360(1997).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC lipoamide dehydrogenase (E3).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
CC acetyl-dihydrolipoamide.
CC -!- COFACTOR: Contains 3 covalently bound lipoyl cofactors (By
CC similarity).
CC -!- SUBUNIT: Forms a 24-polypeptide structural core with octahedral
CC symmetry.
CC -!- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
CC -!- SIMILARITY: Contains 3 lipoyl-binding domains.
CC -----
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CC -----
CC EMBL; X12455; CAA30987.1; ALT_INIT.
CC PIR; S01017; XXAV.
CC PDB; 1EAA; 31-OCT-93.
CC PDB; 1EAB; 31-OCT-93.
CC PDB; 1EAC; 31-OCT-93.
CC PDB; 1EAD; 31-OCT-93.
CC PDB; 1EAE; 31-OCT-93.
CC PDB; 1EAF; 31-OCT-93.
CC PDB; 1EAY; 12-MAR-97.
CC PDB; 1IYU; 12-MAR-97.
CC PDB; 1DPC; 20-APR-95.
CC PDB; 1DPE; 20-APR-95.
CC PDB; 1DDP; 20-APR-95.
CC InterPro; IPR001078; 2Oxoacid_dh.
CC InterPro; IPR006256; Acef.
CC InterPro; IPR000089; Biotin_lipoyl.
CC InterPro; IPR004167; E3_binding.
CC InterPro; IPR003016; Lipoyl_BS.
CC Pfam; PF00198; 2-oxoacid_dh; 1.
CC Pfam; PF00364; biotin_lipoyl; 3.
CC Pfam; PF02817; e3_binding; 1.
CC ProDom; PD001115; 2Oxoacid_dh; 1.

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DR TIGREMS: TIGR01348; PDHac trf\_long; 1.  
DR PROSITE; PS00189; LIPOYL; 3.  
KW Glycolysis; Transferase; Acyltransferase; Repeat; Lipoyl;  
3D-structure.

FT INIT MET 0  
FT DOMAIN 1 326 LIPOYL BINDING.  
FT DOMAIN 327 380 EL/E3 BINDING.  
FT DOMAIN 381 637 CATALYTIC.  
FT BINDING 39 39 LIPOYL (POTENTIAL).  
FT BINDING 156 156 LIPOYL (POTENTIAL).  
FT BINDING 261 261 LIPOYL (POTENTIAL).  
FT REPEAT 1 115  
FT REPEAT 116 220  
FT REPEAT 221 326  
FT ACT\_SITE 610 610  
FT STRAND 2 5  
FT STRAND 12 18  
FT TURN 22 23  
FT STRAND 25 25  
FT STRAND 31 36  
FT STRAND 41 45  
FT STRAND 51 55  
FT TURN 59 60  
FT STRAND 62 64  
FT TURN 65 66  
FT STRAND 68 73  
FT HELIX 403 406  
FT HELIX 416 431  
FT STRAND 434 442  
FT HELIX 444 452  
FT TURN 453 453  
FT HELIX 454 459  
FT TURN 460 461  
FT HELIX 466 480  
FT HELIX 482 484  
FT STRAND 490 491  
FT TURN 495 497  
FT STRAND 503 505  
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FT STRAND 512 514  
FT STRAND 517 518  
FT HELIX 521 523  
FT HELIX 526 541  
FT TURN 542 543  
FT HELIX 547 550  
FT STRAND 555 559  
FT TURN 561 563  
FT TURN 574 575  
FT STRAND 578 582  
FT STRAND 586 591  
FT STRAND 596 609  
FT TURN 610 612  
FT HELIX 615 630  
FT HELIX 632 637  
SQ SEQUENCE 637 AA; 64913 MW; D6063B4A5A385F84 CRC64;

Query Match 29.8%; Score 102; DB 1; Length 637;  
Best Local Similarity 36.7%; Pred. No. 0.014;  
Matches 22; Conservative 15; Mismatches 23; Indels 0; Gaps 0;

QY 10 GTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTQGVKVLVKERDAVQGGGLIKI 69  
DB 13 GEVIELLVKTGDLIEVEQGLVLESAKASMEVSPKAGVKSUSVKGDKLKEGDALIEL 72

RESULT 40  
BCCP SOYBN  
ID BCCP SOYBN STANDARD; PRT; 262 AA.  
AC Q42783;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Biotin carboxyl carrier protein of acetyl-CoA carboxylase, chloroplast  
DE Precursor (BCCP).  
GN ACCB-1.  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RA STRAIN=cv. Resnik;  
RC Reverdatto S.V., Beilinson V., Neilsen N.C.;  
RT "Characterization of a cDNA clone encoding a BCCP subunit of acetyl-CoA carboxylase from soybean".  
RL (in) Plant Gene Register PGR96-040.  
CC -!- FUNCTION: This protein is a component of the acetyl coenzyme A carboxylase complex; first, biotin carboxylase catalyzes the carboxylation of the carrier protein and then the transcarboxylase transfers the carboxyl group to form malonyl-CoA.  
CC -!- PATHWAY: long-chain fatty acid biosynthesis; first step.  
CC -!- SUBCELLULAR LOCATION: Chloroplast.  
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CC  
DR EMBL; U40666; AAB67836.1; -.  
DR PIR; T06600; T06600.  
DR HSSP; P02905; 3BDQ.  
DR InterPro; IPR001249; AcCoA\_biotinCC.  
DR InterPro; IPR001882; Biotin\_BS.  
DR InterPro; IPR000089; Biotin\_lipoyl.  
DR Pfam; PF00364; biotin\_lipoyl; 1.  
DR PRINTS; PR01071; AC0ABIOTINCC.  
DR TIGRFAMs; TIGR00531; BCCP; 1.  
DR PROSITE; PS00188; BIOTIN; 1.  
KW Fatty acid biosynthesis; Biotin; Chloroplast; Transit peptide.  
FT TRANSIT 1 47 CHLOROPLAST.  
FT CHAIN 48 262 BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-CoA CARBOXYLASE.  
FT BINDING 227 227 BIOTIN (BY SIMILARITY).  
FT SEQUENCE 262 AA; 27657 MW; 79B273BD8B87DF48 CRC64;

Query Match 29.7%; Score 101.5; DB 1; Length 262;  
Best Local Similarity 34.4%; Pred. No. 0.0069;  
Matches 22; Conservative 14; Mismatches 21; Indels 7; Gaps 1;

QY 4 IPAPLAGTVSK-----ILVKEGTVKAGQTVLVLEAMKMETEINAPTQGVKVLVKE 56  
DB 188 LXSPWAGTYRSPAPGEPSPFVKGVKRGQVVCIIIEAMKLNIEADQSGLIVEIVAE 247

QY 57 RDAV 60  
DB 248 AKSV 251

Search completed: March 3, 2004, 10:29:44  
Job time : 8.29167 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 3, 2004, 10:25:29 ; Search time 25.8854 Seconds  
(without alignments)  
853.232 Million cell updates/sec

Title: US-09-987-485A-2

Perfect score: 342

Sequence: 1 EGEIPAPLAGTVSKILVKEG.....KVLVKERDAVQGGGLIKIG 70

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	214	62.6	120	16 Q8RF4	Q8rf4 corynebacte
2	195	57.0	145	17 Q9V0A6	Q9v0a6 pyrococcus
3	189	55.3	149	17 Q59021	Q59021 pyrococcus
4	181	52.9	144	17 Q8U303	Q8u303 pyrococcus
5	180	52.6	571	17 Q58564	Q58564 pyrococcus
6	178	52.0	140	17 Q28067	Q28067 archaeoglob
7	178	52.0	986	16 Q89118	Q89118 clostridium
8	174	50.9	655	16 Q67484	Q67484 aquifex ao
9	174	50.9	984	2 Q9XBJ1	Q9xbj1 bacillus ce
10	174	50.9	1148	16 Q81MT6	Q81mt6 bacillus an
11	174	50.9	1148	16 Q819M9	Q819m9 bacillus ce
12	170	49.7	186	17 Q37VY7	Q37vy7 sulfobolus
13	167	48.8	134	16 Q9WZB6	Q9wzb6 thermotoga
14	167	48.8	596	2 Q48826	Q48826 legionella
15	167	48.8	1144	16 Q97FR7	Q97fr7 clostridium
16	165	48.2	167	1 Q8J2Z3	Q8j2z3 metallospha

17	165	48.2	1144	16 Q88VC5	Q88vc5 lactobacill
18	164	48.0	597	16 Q9KH1	Q9khl1 vibrio chol
19	163	47.7	599	16 Q9PF00	Q9pf00 campylobact
20	161	47.1	142	17 Q28194	Q28194 archaeoglob
21	160	46.8	602	16 Q87U07	Q87u07 pseudomonas
22	159.5	46.6	576	16 Q8U917	Q8u917 agrobacteri
23	159	46.5	144	16 Q8A737	Q8a737 bacteroides
24	159	46.5	602	16 Q88C37	Q88c37 pseudomonas
25	159	46.5	665	16 Q92H13	Q92h13 rickettsia
26	158	46.2	169	17 Q974R8	Q974r8 sulfobolus
27	158	46.2	607	16 Q9HTD1	Q9htd1 pseudomonas
28	157	45.9	1146	16 Q92CW1	Q92cw1 listeria in
29	157	45.9	1146	16 Q8Y846	Q8y846 listeria mo
30	157	45.9	1150	16 Q9K9M0	Q9k9m0 bacillus ha
31	156.5	45.8	1140	2 Q8L264	Q8l264 corynebacte
32	156	45.6	116	16 Q99ZL6	Q99zl6 streptococc
33	156	45.6	116	16 Q8K7G1	Q8k7g1 streptococc
34	155.5	45.5	1139	2 Q8RQL2	Q8rql2 corynebacte
35	155.5	45.5	1140	16 Q54587	Q54587 corynebacte
36	155.5	45.5	1168	16 Q8PRQ0	Q8prq0 corynebacte
37	155	45.3	116	16 Q8P104	Q8p104 streptococc
38	153	44.7	135	16 Q8RAJ2	Q8raj2 thermoanaer
39	153	44.7	620	16 Q67544	Q67544 aquifex ao
40	152	44.4	167	1 Q52603	Q52603 sulfobolus
41	152	44.4	167	1 Q87714	Q87714 acidianus b
42	152	44.4	436	10 Q40121	Q40121 lycopersico
43	152	44.4	595	16 Q87LR7	Q87lr7 vibrio para
44	151	44.2	157	16 Q8K630	Q8k630 streptococc
45	151	44.2	166	16 Q99YD8	Q99yd8 streptococc

#### ALIGNMENTS

#### RESULT 1

Q8RF4 PRELIMINARY; PRT; 120 AA.

AC Q8RF4; 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 25, Last annotation update)

DE Putative biotin carboxyl carrier protein.

GN CE0807.

OS Corynebacterium efficiens.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.

OX NCBI\_TaxID=152794;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;

RA Kawarayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,

RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,

RA Usuda Y., Sugimoto S.;

RT "The entire genomic sequence of Corynebacterium efficiens YS-314."

RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP005216; BAC17617.1; -

DR GO; GO:0009374; F:biotin binding; IEA.

DR InterPro; IPR001882; Biotin\_BS.

DR InterPro; IPR000089; Biotin\_lipoyl.

DR Pfam; PF00364; biotin\_lipoyl; 1.

DR PROSITE; PS00188; BIOTIN; 1.

KW Complete proteome.

SQ SEQUENCE 120 AA; 12298 MW; 4C36B4B41C969E5 CRC64;

Query Match 62.6%; Score 214; DB 16; Length 120;  
Best Local Similarity 68.2%; Pred. No. 1.1e-14;  
Matches 45; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETETINAPTDCGKVKLVKRDVCGG 63  
DB 54 VVAPLAGSVFKILVAEGDTIAGQVLLVLEAMKMETETITAPSAGVGVAINVKEGAVCGG 113  
QY 64 QGLIKI 69

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Db 114 QSLIEI 119
| ||:|
RL DNA Res. 5:55-76(1998).
DR EMBL; AP000005; BAA30387.1; -.
DR PIR; A71074; A71074.
DR HSSP; P10802; 1IYU.
DR GO; GO:0009374; F:biotin binding; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; Biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Complete proteome.
SQ SEQUENCE 149 AA; 15985 MW; 1C3AA5F47E6BA6F1 CRC64;

Query Match 55.3%; Score 189; DB 17; Length 149;
Best Local Similarity 54.3%; Pred. No. 5.7e-12;
Matches 38; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGT VSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVLVKERDAV 60
Db 80 ENVVSAPMPGKVLRLVLRVGVDEVRVYGGLLILEAMKMEIIPSPRDGVVVKILVKEGEAV 139
QY 61 QGGQGLIKIG 70
Db 140 DTGTPLELG 149

RESULT 4
Q8U303 PRELIMINARY; PRT; 144 AA.
AC Q8U303;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Methylnalonyl-CoA decarboxylase gamma chain.
GN PF0673.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AEO10188; AAL80797.1;
DR GO; GO:0009374; F:biotin binding; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; Biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Complete proteome.
SQ SEQUENCE 144 AA; 15315 MW; 422C96A8ED809C6A CRC64;

Query Match 52.9%; Score 181; DB 17; Length 144;
Best Local Similarity 55.2%; Pred. No. 3.7e-11;
Matches 37; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 4 IPAPLAGT VSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVLVKERDAVQGG 63
Db 78 VTAPMPGKILVSEGQRTVYGGLLILEAMKMEIIPSPKDVVVKIYVKEGDTVDTG 137
QY 64 QGLIKIG 70
Db 138 QPLIELG 144

RESULT 5
Q58564 PRELIMINARY; PRT; 571 AA.
ID Q58564
AC Q58564;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Query Match 57.0%; Score 195; DB 17; Length 145;
Best Local Similarity 58.8%; Pred. No. 1.3e-12;
Matches 41; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGT VSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVLVKERDAV 60
Db 76 ENVVTAPMPGKVLRLVLRVGVDEVRVYGGLLILEAMKMEIIPAPRDGVVVKILVKEGDAV 135
QY 61 QGGQGLIKIG 70
Db 136 DTGTPLELG 145

RESULT 3
Q59021 PRELIMINARY; PRT; 149 AA.
AC Q59021;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 149AA long hypothetical methylnalonyl-CoA decarboxylase gamma chain.
GN PH1284.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RA Kwarabavasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
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DE 571AA long hypothetical oxaloacetate decarboxylase alpha chain.  
 GN PF0834.  
 OS Pyrococcus horikoshii.  
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
 OC Pyrococcus.  
 OX NCBI\_TaxID=53953;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=OT3;  
 RX MEDLINE=98344137; PubMed=9679194;  
 RA Kawarayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,  
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,  
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,  
 RA Funahashi T., Tanaka K., Kudoh Y., Yamazaki J., Kushiida N., Ogunchi A.,  
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,  
 RA Mauchi Y., Shiruya H., Kikuchi H.;  
 RT "Complete sequence and gene organization of the genome of a hyper-  
 thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";  
 RL DNA Res. 5:55-76(1998).  
 DR EMBL; AF000003; BAA29928.1; -.  
 DR PIR; F71133; F71133.  
 DR HSP; P02905; 1BD0.  
 DR GO; GO:0009374; F:biotin binding; IEA.  
 DR GO; GO:0003824; F:catalytic activity; IEA.  
 DR GO; GO:0008948; F:oxaloacetate decarboxylase activity; IEA.  
 DR GO; GO:0006814; P:sodium ion transport; IEA.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR InterPro; IPR000891; HMGL-like.  
 DR InterPro; IPR005776; OADA.  
 DR InterPro; IPR003379; PYC OADA.  
 DR Pfam; PF00364; biotin\_lipoyl; 1.  
 DR Pfam; PF00682; HMGL-like; 1.  
 DR Pfam; PF02436; PYC OADA; 1.  
 DR TIGRFAMs; TIGR01108; oada; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 571 AA; 64748 MW; B308B0B1C0E5B103 CRC64;  
 Query Match 52.6%; Score 180; DB 17; Length 571;  
 Best Local Similarity 54.5%; Pred. No. 2.3e-10;  
 Matches 36; Conservative 14; Mismatches 16; Indels 0; Gaps 0;  
 Qy 4 IPAPLAGTGVSKLVKGGDTVKGAGTVLVLEAMKMETEINAPTDGKVKVLRKRDVQGG 63  
 Db 505 VSADMPGKVLVRVGVGVGGVGLLVLEAMKMETEINAPTDGKVKVLRKRDVQGG 63  
 Qy 64 QGLIKI 69  
 Db 565 QPLIEL 570  
 RESULT 6  
 Q28067 ID O28067 PRELIMINARY; PRT; 140 AA.  
 AC O28067;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Methylmalonyl-CoA decarboxylase, biotin carboxyl carrier subunit  
 DE (MWDG).  
 GN AF2216.  
 OS Archaeoglobus fulgidus.  
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;  
 OC Archaeoglobaceae; Archaeoglobus.  
 OX NCBI\_TaxID=2234;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;  
 RX MEDLINE=98049343; PubMed=9389475;  
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,  
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,  
 RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,  
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,  
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,  
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uterback T.,  
 RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,  
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,  
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,  
 RA Venter J.C.;  
 RT "The complete genome sequence of the hyperthermophilic, sulphate-  
 reducing archaeon Archaeoglobus fulgidus.";  
 RL Nature 390:364-370(1997).  
 DR EMBL; AE000952; AAB89036.1; -.  
 DR PIR; H69526; H69526.  
 DR HSP; P20708; 1GHJ.  
 DR TIGR; AF2216; -.  
 DR GO; GO:0009374; F:biotin binding; IEA.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR Pfam; PF00364; biotin\_lipoyl; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 140 AA; 15686 MW; 30B449C45489C14A CRC64;  
 Query Match 52.0%; Score 178; DB 17; Length 140;  
 Best Local Similarity 54.7%; Pred. No. 7.5e-11;  
 Matches 35; Conservative 13; Mismatches 16; Indels 0; Gaps 0;  
 Qy 4 IPAPLAGTGVSKLVKGGDTVKGAGTVLVLEAMKMETEINAPTDGKVKVLRKRDVQGG 63  
 Db 74 ITAPMAGVTIKLVKGGKVKAGETVLIIEMKMNFIAPDEGEIAEIVVKGDKVASG 133  
 Qy 64 QGLI 67  
 Db 134 DVLV 137  
 RESULT 7  
 Q891Y8 ID Q891Y8 PRELIMINARY; PRT; 986 AA.  
 AC Q891Y8;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Pyruvate carboxylase (EC 6.4.1.1).  
 GN CFC02224.  
 OS Clostridium tetani.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Massachusetts / E88;  
 RX MEDLINE=22457253; PubMed=12552129;  
 RA Bruggemann H., Baumer S., Fricke W.F., Wierze A., Liesegang H.,  
 RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,  
 RA Gottschalk G.;  
 RT "The genome sequence of Clostridium tetani, the causative agent of  
 tetanus disease.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).  
 DR EMBL; AE015943; AA036707.1; -.  
 DR GO; GO:000524; F:ATP binding; IEA.  
 DR GO; GO:0009374; F:biotin binding; IEA.  
 DR GO; GO:0016874; F:ligase activity; IEA.  
 DR GO; GO:0004736; F:pyruvate carboxylase activity; IEA.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR InterPro; IPR005482; Biotin\_carb C.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR InterPro; IPR005479; CPase\_L\_D2.  
 DR InterPro; IPR000891; HMGL-like.  
 DR InterPro; IPR003379; PYC OADA.  
 DR Pfam; PF02785; Biotin\_carb C; 1.  
 DR Pfam; PF00364; biotin\_lipoyl; 1.  
 DR Pfam; PF02786; CPase\_L\_D2; 1.

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DR Pfam; PF00682; HMGU-like; 1.
DR Pfam; PF02436; PYC OADA; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
DR KW Ligase; Complete proteome.
SQ SEQUENCE 986 AA; 110669 MW; 8825F618B0A4B219 CRC64;

Query Match 52.0%; Score 178; DB 16; Length 986;
Best Local Similarity 52.2%; Pred. No. 7e-10;
Matches 36; Conservative 13; Mismatches 20; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPDTGKVKVVKERDAV 60
Db 916 KSGIGASIPGNISKILKEGDTVNGKDRIVAEAMKMETVSTVGTGVKKVIFVKEQV 975
QY 61 QGGQGLIKI 69
Db 976 KVGQGLIIKI 984

RESULT 8
O67484 PRELIMINARY; PRT; 655 AA.
AC O67484;
DT 01-AUG-1998 (T-EMBLrel. 07, Created)
DT 01-AUG-1998 (T-EMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Pyruvate carboxylase C-terminal domain.
GN PYCA OR AQ_1520.
OS Aquifex aeolicus.
OC Bacteria; Aquificae;
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.,
RT "the complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus";
RL Nature 392:353-358 (1998).
DR EMBL; AE000744; AAC07445.1; -.
DR PIR; B70432; B70432.
DR HSP; P02905; IBD0.
DR GO; GO:000374; F:biotin binding; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC OADA.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00682; HMGU-like; 1.
DR Pfam; PF02436; PYC OADA; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR Pyruvate; Complete proteome.
SQ SEQUENCE 655 AA; 73612 MW; 2839436F6BFE05D6 CRC64;

Query Match 50.9%; Score 174; DB 16; Length 655;
Best Local Similarity 50.0%; Pred. No. 1.1e-09;
Matches 34; Conservative 13; Mismatches 21; Indels 0; Gaps 0;

QY 2 GEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPDTGKVKVVKERDAVQ 61
Db 578 GDTVPFPGKVKVILVKEGEPVQGGQIVATVEAMKMETVSTVGTGVKKVIFVKEQV 637
QY 62 GGQGLIKI 69
Db 638 PDQAIMRI 645

RESULT 9
Q9XBJ1 PRELIMINARY; PRT; 984 AA.
AC Q9XBJ1;
DT 01-NOV-1999 (T-EMBLrel. 12, Created)
DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Pyruvate carboxylase (EC 6.4.1.1) (Fragment).
GN PYCA.
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10987;
RA Oktad O.A., Hegna I., Lindbaeck T., Rishovd A.L., Kolsto A.B.;
RT "genome organisation is not conserved between Bacillus cereus and
RT Bacillus subtilis.";
RL Microbiology 145:621-631 (1999).
DR EMBL; AJ010111; CAB40604.1; -.
DR PIR; T44608; T44608.
DR HSP; P24182; LDV2.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004736; F:pyruvate carboxylase activity; IEA.
DR GO; GO:0006094; P:gluconeogenesis; IEA.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC OADA.
DR InterPro; IPR005930; Pyruv. carbox.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF02786; CPase_L_D2; 1.
DR Pfam; PF00682; HMGU-like; 1.
DR Pfam; PF02436; PYC OADA; 1.
DR TIGRFAMs; TIGR01235; pyruv. carbox; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
DR KW Ligase.
FT NON_TER 1 1
SQ SEQUENCE 984 AA; 110135 MW; 7AB52F8D453A147D CRC64;

Query Match 50.9%; Score 174; DB 2; Length 984;
Best Local Similarity 53.0%; Pred. No. 1.8e-09;
Matches 35; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 4 IPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPDTGKVKVVKERDAVQGG 63
Db 917 ISATMEPTGVKVVVKEGDEVKKGDSMAITAMKMETTVQAPFNKGVKVVNDGDAIQG 976
QY 64 QGLIKI 69
Db 977 DLJIEL 982

RESULT 10
Q81MT6 PRELIMINARY; PRT; 1148 AA.
AC Q81MT6;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Pyruvate carboxylase.
GN PYC OR BA4157.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,

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RA Holtzapfel E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,  
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,  
RA DeBoy R.T., Madupu R., Daugherty S.C., Durkin A.S., Haft D.H.,  
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,  
RA Benton J.L., Mahmoud Y., Jiang L., Wang L., Weidman J.F.,  
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Niemeyer W.C.,  
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,  
RA Thomsen B., Friedlander A.M., Kohler T.M., Hanna P.C., Kolsto A.-B.,  
RA Fraser C.M.;  
RT "The genome sequence of *Bacillus anthracis* Ames and comparison to  
RT closely related bacteria";  
RL Nature 423:81-86(2003).  
DR EMBL: AE017037; AAP27881.1; --  
DR TIGR: BA4157; --  
DR GO: GO:0005737; C:cytoplasm; IEA.  
DR GO: GO:0005524; F:ATP binding; IEA.  
DR GO: GO:0016874; F:ligase activity; IEA.  
DR GO: GO:0004736; F:pyruvate carboxylase activity; IEA.  
DR GO: GO:0006034; P:gluconeogenesis; IEA.  
DR GO: GO:0008152; P:metabolism; IEA.  
DR InterPro: IPR005482; Biotin carb. C.  
DR InterPro: IPR000089; Biotin lipoyl.  
DR InterPro: IPR005479; CPase L D2.  
DR InterPro: IPR005481; CPase L N.  
DR InterPro: IPR000891; HMGL-like.  
DR InterPro: IPR003379; PYC OADA.  
DR InterPro: IPR005930; Pyruv. carbox.  
DR Pfam: PF02785; Biotin carb. C; 1.  
DR Pfam: PF00364; biotin lipoyl; 1.  
DR Pfam: PF00289; CPase L chain; 1.  
DR Pfam: PF02786; CPase L D2; 1.  
DR Pfam: PF00682; HMGL-like; 1.  
DR Pfam: PF02436; PYC OADA; 1.  
DR TIGRFAMs: TIGR01235; pyruv. carbox; 1.  
DR PROSITE: PS00866; CPASE 1; 1.  
DR InterPro: IPR005481; CPase L N.  
DR InterPro: IPR000891; HMGL-like.  
DR InterPro: IPR003379; PYC OADA.  
DR InterPro: IPR005930; Pyruv. carbox.  
DR Pfam: PF02785; Biotin carb. C; 1.  
DR Pfam: PF00364; biotin lipoyl; 1.  
DR Pfam: PF00289; CPase L chain; 1.  
DR Pfam: PF02786; CPase L D2; 1.  
DR Pfam: PF00682; HMGL-like; 1.  
DR Pfam: PF02436; PYC OADA; 1.  
DR TIGRFAMs: TIGR01235; pyruv. carbox; 1.  
DR PROSITE: PS00866; CPASE 1; 1.  
DR PROSITE: PS00867; CPASE 2; 1.  
KW Pyruvate; Complete proteome.  
SQ SEQUENCE 1148 AA; 128573 MW; 57B97F8D9D1287BF CRC64;

Query Match 50.9%; Score 174; DB 16; Length 1148;  
Best Local Similarity 53.0%; Pred. No. 2.2e-09;  
Matches 35; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

Qy 4 IPAPLACTVSKILVKEGDTVKGAGTQVLVLEAKMTEINAPTCDGKVEKLVKEDAVOGG 63  
Db 1081 ISATMPGTVIKVVKEGDEKVGDSMAITAEAKMETTVQAFNGKVKVYVNDGAIQTG 1140  
Qy 64 QGLIKI 69  
Db 1141 DLLIEL 1146

RESULT 11  
Q819M9 PRELIMINARY; PRT; 1148 AA.  
ID Q819M9  
AC Q819M9  
DT 01-JUN-2003 (TRENBLrel. 24, Created)  
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Pyruvate carboxylase (EC 6.4.1.1).  
GN BC3947.  
OS *Bacillus cereus* (strain ATCC 14579 / DSM 31).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=226900;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22608415; PubMed=12721630;  
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelson B.,  
RA Kapral V., Bhattacharya A., Renik G., Mikhailova N., Lapidus A.,  
RA Chu L., Mazur M., Goldsman E., Larsen N., D'Souza M., Walunas T.,  
RA Grechkin Y., Pusch G., Hasekorn R., Fonstein M., Ehrlich S.D.,  
RA Overbeek R., Kyrpides N;  
RT "Genome sequence of *Bacillus cereus* and comparative analysis with

RT *Bacillus anthracis*";  
RL Nature 423:87-91(2003).  
DR EMBL: AE017010; AAP10867.1; --  
DR GO: GO:0005737; C:cytoplasm; IEA.  
DR GO: GO:0005524; F:ATP binding; IEA.  
DR GO: GO:0016874; F:ligase activity; IEA.  
DR GO: GO:0004736; F:pyruvate carboxylase activity; IEA.  
DR GO: GO:0006034; P:gluconeogenesis; IEA.  
DR GO: GO:0008152; P:metabolism; IEA.  
DR InterPro: IPR005482; Biotin carb. C.  
DR InterPro: IPR000089; Biotin lipoyl.  
DR InterPro: IPR005479; CPase L D2.  
DR InterPro: IPR005481; CPase L N.  
DR InterPro: IPR000891; HMGL-like.  
DR InterPro: IPR003379; PYC OADA.  
DR InterPro: IPR005930; Pyruv. carbox.  
DR Pfam: PF02785; Biotin carb. C; 1.  
DR Pfam: PF00364; biotin lipoyl; 1.  
DR Pfam: PF00289; CPase L chain; 1.  
DR Pfam: PF02786; CPase L D2; 1.  
DR Pfam: PF00682; HMGL-like; 1.  
DR Pfam: PF02436; PYC OADA; 1.  
DR TIGRFAMs: TIGR01235; pyruv. carbox; 1.  
DR PROSITE: PS00866; CPASE 1; 1.  
DR PROSITE: PS00867; CPASE 2; 1.  
KW Ligase; Pyruvate; Complete proteome.  
SQ SEQUENCE 1148 AA; 128442 MW; E5CC5BA99D8E191 CRC64;

Query Match 50.9%; Score 174; DB 16; Length 1148;  
Best Local Similarity 53.0%; Pred. No. 2.2e-09;  
Matches 35; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

Qy 4 IPAPLACTVSKILVKEGDTVKGAGTQVLVLEAKMTEINAPTCDGKVEKLVKEDAVOGG 63  
Db 1081 ISATMPGTVIKVVKEGDEKVGDSMAITAEAKMETTVQAFNGKVKVYVNDGAIQTG 1140  
Qy 64 QGLIKI 69  
Db 1141 DLLIEL 1146

RESULT 12  
Q97VV7 PRELIMINARY; PRT; 186 AA.  
ID Q97VV7  
AC Q97VV7  
DT 01-OCT-2001 (TRENBLrel. 18, Created)  
DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Biotin carboxyl carrier protein of propionyl-CoA carboxylase beta subunit (EC 6.4.1.3).  
GN SSO2464.  
OS *Sulfolobus solfataricus*.  
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
OC *Sulfolobus*.  
OX NCBI\_TaxID=2287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 35092 / DSM 1617 / P2;  
RX MEDLINE=21332296; PubMed=11427726;  
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,  
RA Aweez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,  
RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,  
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,  
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,  
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,  
RA Garrett R.A., Ragan M.A., Senses C.W., Van der Oost J.;  
RT "The complete genome of the crenarchaeon *Sulfolobus solfataricus* P2.";  
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).  
DR EMBL: AE006845; AA42603.1; --  
DR PIR: D90418; D90418.  
DR GO: GO:0009374; F:biotin binding; IEA.  
DR GO: GO:0016874; F:ligase activity; IEA.  
DR GO: GO:0004658; F:propionyl-CoA carboxylase activity; IEA.

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DR InterPro; IPR001882; Biotin BS
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; Biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR Ligase; Complete proteome.
SQ SEQUENCE 186 AA; 21166 MW; DB26587C39883B08 CRC64;

Query Match 49.7%; Score 170; DB 17; Length 186;
Best Local Similarity 55.1%; Pred. No. 7e-10;
Matches 38; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGVSVKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
DB 117 EGEIVSPFGVVKIRVKEGDAVNGQPLLSIEAMKAETVLISSPGIGVQKILKEGGV 176
QY 61 QGGGLIKI 69
DB 177 KKGDIILVI 185

RESULT 13
Q9WZH6 PRELIMINARY; PRT; 134 AA.
AC Q9WZH6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Propionyl-CoA carboxylase, gamma subunit.
GN TM0717.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
EN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=95287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Hart D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RA "Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima."
RL Nature 393:323-329 (1999).
DR EMBL; AE001743; AAD35739.1; -.
DR PIR; C72341; C72341.
DR HSSP; P02905; 1BDO.
DR TIGR; TM0717; -.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
KW Complete proteome.
SQ SEQUENCE 134 AA; 15131 MW; A3BFBAACE8574EC1 CRC64;

Query Match 48.8%; Score 167; DB 16; Length 134;
Best Local Similarity 51.8%; Pred. No. 9.9e-10;
Matches 34; Conservative 12; Mismatches 20; Indels 0; Gaps 0;

QY 4 IPAPLAGVSVKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGG 63
DB 68 VKAPMAGVVLVVKEGQVNVGDKLLVFEAMKMEINELQSEFSGTVKEILVKEGDNITG 127
QY 64 QGLIKI 69
DB 128 QILMKI 133

RESULT 14
Q48826 PRELIMINARY; PRT; 596 AA.
AC Q48826;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DR InterPro; IPR001882; Biotin BS
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; Biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR Ligase; Complete proteome.
SQ SEQUENCE 186 AA; 21166 MW; DB26587C39883B08 CRC64;

Query Match 49.7%; Score 170; DB 17; Length 186;
Best Local Similarity 55.1%; Pred. No. 7e-10;
Matches 38; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGVSVKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAV 60
DB 117 EGEIVSPFGVVKIRVKEGDAVNGQPLLSIEAMKAETVLISSPGIGVQKILKEGGV 176
QY 61 QGGGLIKI 69
DB 177 KKGDIILVI 185

RESULT 13
Q9WZH6 PRELIMINARY; PRT; 134 AA.
AC Q9WZH6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Propionyl-CoA carboxylase, gamma subunit.
GN TM0717.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
EN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=95287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Hart D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RA "Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima."
RL Nature 393:323-329 (1999).
DR EMBL; AE001743; AAD35739.1; -.
DR PIR; C72341; C72341.
DR HSSP; P02905; 1BDO.
DR TIGR; TM0717; -.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
KW Complete proteome.
SQ SEQUENCE 134 AA; 15131 MW; A3BFBAACE8574EC1 CRC64;

Query Match 48.8%; Score 167; DB 2; Length 596;
Best Local Similarity 51.5%; Pred. No. 5.5e-09;
Matches 35; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 2 GEIPAPLAGVSVKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQ 61
DB 526 GDITVAIPGSIILHVSAGDEVKAGAVLVIEAMKMETEIKAPANGVVAIILCQKQKVT 585
QY 62 GGGLIKI 69
DB 586 PGQVLIRV 593

RESULT 15
Q97FR7 PRELIMINARY; PRT; 1144 AA.
AC Q97FR7;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pyruvate carboxylase, PYCA.
GN CAC2660.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
EN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Onelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatunov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;

```

"Genome sequence and comparative analysis of the solvent-producing bacterium *Clostridium acetobutylicum*.";

RT J. Bacteriol. 193:4823-4838(2001).  
 RL EMBL; AB007763; AAK0607.1; -.  
 DR PIR; D97227; D97227.  
 DR GO; GO:0005737; C:cytoplasm; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0009374; F:biotin binding; IEA.  
 DR GO; GO:0004086; F:carbamoyl-phosphate synthase activity; IEA.  
 DR GO; GO:0016874; F:ligase activity; IEA.  
 DR GO; GO:0004736; F:pyruvate carboxylase activity; IEA.  
 DR GO; GO:0006094; P:gluconeogenesis; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR InterPro; IPR005482; Biotin\_carb\_C.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR InterPro; IPR005483; CPase\_L.  
 DR InterPro; IPR005479; CPase\_L\_D2.  
 DR InterPro; IPR005481; CPase\_L\_N.  
 DR InterPro; IPR000891; HMGL-like.  
 DR InterPro; IPR003379; PYC\_OADA.  
 DR InterPro; IPR005330; Pyruv\_carbox.  
 DR Pfam; PF02785; Biotin\_carb\_C; 1.  
 DR Pfam; PF00364; Biotin\_lipoyl; 1.  
 DR Pfam; PF00289; CPase\_L; 1.  
 DR Pfam; PF02786; CPase\_L\_D2; 1.  
 DR Pfam; PF00682; HMGL-like; 1.  
 DR Pfam; PF02436; PYC\_OADA; 1.  
 DR PRINTS; PRO0098; CPASE.  
 DR TIGRFAMs; TIGR01235; pyruv\_carbox; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 DR PROSITE; PS00866; CPASE\_1; 1.  
 DR PROSITE; PS00867; CPASE\_2; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 1144 AA; 127709 MW; 519FA29A8008F326 CRC64;  
 Query Match 48.8%; Score 167; DB 16; Length 1144;  
 Best Local Similarity 50.7%; Pred. No. 1.2e-08;  
 Matches 34; Conservative 11; Mismatches 22; Indels 0; Gaps 0;  
 QY 3 EIPAPLAGTAVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQGVKVKVLERDAVQ 62  
 DB 1077 EIGASIPGVNVKVFVKPGDKVKGSLMVEIAMKMETVSVSDGTGVGIFVKGQDVQS 1136  
 QY 63 QGGGLIKI 69  
 DB 1137 GQLLVKL 1143  
 RESULT 16  
 Q8J2Z3 Q8J2Z3 PRELIMINARY; PRT; 167 AA.  
 AC Q8J2Z3;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Biotin carrier protein.  
 GN ACCE.  
 OS Metallosphaera sedula.  
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
 OC Metallosphaera.  
 OC NCBI\_TaxID=43687;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hugler M., Krieger R.S., Jahn M., Fuchs G.;  
 RT "Characterization of Acetyl-CoA/Propionyl-CoA Carboxylase in  
 RT Metallosphaera sedula - Carboxylating Enzyme in the 3-  
 RT Hydroxypropionate Cycle for Autotrophic Carbon Fixation.";  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBS databases.  
 DR EMBL; AF461116; AAO15573.1; -.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR Pfam; PF00364; Biotin\_lipoyl; 1.  
 SQ SEQUENCE 167 AA; 18634 MW; FC4504CE2EE7D91C CRC64;

Query Match 48.2%; Score 165; DB 1; Length 167;  
 Best Local Similarity 52.2%; Pred. No. 2.1e-09;  
 Matches 36; Conservative 10; Mismatches 23; Indels 0; Gaps 0;  
 QY 1 EGEIPAPLAGTAVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQGVKVKVLERDAV 60  
 DB 98 EGEVLSPLQGRVVQVRVKEGDAVNVKGQPLLSEAMKSETIVSPLISGLVKEVVKVKGQGV 157  
 QY 61 QGGGLIKI 69  
 DB 158 KKGDLVVI 166  
 RESULT 17  
 Q88VCS Q88VCS PRELIMINARY; PRT; 1144 AA.  
 AC Q88VCS;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Pyruvate carboxylase (EC 6.4.1.1).  
 GN PYCA OR LP 2136.  
 OS Lactobacillus plantarum.  
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
 OC Lactobacillus.  
 OC NCBI\_TaxID=1590;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NCIMB 8826 / WCFS1;  
 RX MEDLINE=22480296; PubMed=12566566;  
 RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,  
 RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,  
 RA Pijfs M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,  
 RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,  
 RA De Vos W.M., Siezen R.J.;  
 RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).  
 DR EMBL; AL035258; CAB64497.1; -.  
 DR GO; GO:0005224; F:ATP binding; IEA.  
 DR GO; GO:0008716; F:D-alanine-D-alanine ligase activity; IEA.  
 DR GO; GO:0016874; F:ligase activity; IEA.  
 DR GO; GO:0004736; F:pyruvate carboxylase activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR GO; GO:0009252; P:peptidoglycan biosynthesis; IEA.  
 DR InterPro; IPR005482; Biotin\_carb\_C.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR InterPro; IPR005479; CPase\_L\_D2.  
 DR InterPro; IPR005481; CPase\_L\_N.  
 DR InterPro; IPR000291; Dala\_lig\_Van.  
 DR InterPro; IPR000891; HMGL-like.  
 DR InterPro; IPR003379; PYC\_OADA.  
 DR Pfam; PF02785; Biotin\_carb\_C; 1.  
 DR Pfam; PF00364; Biotin\_lipoyl; 1.  
 DR Pfam; PF00289; CPase\_L; 1.  
 DR Pfam; PF02786; CPase\_L\_D2; 1.  
 DR Pfam; PF01820; Dala\_Dala\_ligase; 1.  
 DR Pfam; PF00682; HMGL-like; 1.  
 DR Pfam; PF02436; PYC\_OADA; 1.  
 DR PROSITE; PS00866; CPASE\_1; 1.  
 DR PROSITE; PS00867; CPASE\_2; 1.  
 KW Ligase; Complete proteome.  
 SQ SEQUENCE 1144 AA; 127299 MW; BFAP8AD6325DCDF CRC64;

Query Match 48.2%; Score 165; DB 16; Length 1144;  
 Best Local Similarity 49.3%; Pred. No. 1.9e-08;  
 Matches 34; Conservative 13; Mismatches 22; Indels 0; Gaps 0;  
 QY 1 EGEIPAPLAGTAVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTQGVKVKVLERDAV 60  
 DB 1073 EDEVGATMSGVSLKLVKKGQTVKKGEPVLVLEAMKMETTIQAPEDGVIEHYINAGDVI 1132  
 QY 61 QGGGLIKI 69

Putative pyruvate carboxylase B subunit (EC 6.4.1.1).

PYCB OR CJ0933C.

OS Campylobacter jejuni.

OZ Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;

OCC Campylobacteriaceae; Campylobacter.

OX NCBI\_TaxID=197;

RN [1]

RP SEQUENCE FROM N.A.

RR STRAIN=NCTC 11168;

RX MEDLINE=20150912; PubMed=10689204;

RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,

RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,

RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,

RA Whitehead S., Barrrell B.G.;

RA "The genome sequence of the food-borne pathogen Campylobacter jejuni

RT reveals hypervariable sequences.";

RL Nature 403:665-668(2000).

RLL -I- COFACTOR: BIOTIN (BY SIMILARITY).

DR EMBL; AL139076; CAB73190.1; -.

DR PIR; D81367; D81367.

DR HSP; P20708; LGH5.

DR GO; GO:0003974; F:biotin binding; IEA.

DR GO; GO:0003824; F:catalytic activity; IEA.

DR GO; GO:0004736; F:pyruvate carboxylase activity; IEA.

DR InterPro; IPR001882; Biotin\_BS.

DR InterPro; IPR000089; Biotin\_lipoyl.

DR InterPro; IPR000831; HMGL-like

DR Pfam; PF00364; biotin\_lipoyl; 1.

DR Pfam; PF00682; HMGL-like; 1.

DR PROSITE; PS00188; BIOTIN; 1.

KW Biotin; Complete proteome.

SQ SEQUENCE 599 AA; 65833 MW; E5C075E114E40444 CRC64;

Query Match 47.7%; Score 163; DB 16; Length 599;

Best Local Similarity 50.0%; Pred. No. 1.4e-08;

Matches 33; Conservative 13; Mismatches 20; Indels 0; Gaps 0;

QY 1 EGRIAPLAGTSKILVKEGDTVKAGQTVLVLAMKMETEINAFPTDGKVEKLVKERDAV 60  
DB 529 ENEVLAGISGNVFKIYNNEGEVKSQAIVLMEAKMKEIEVNPKDGIILELCIKIGTV 588  
QY 61 QGGQGL 66  
DB 589 NEGEVL 594

RESULT 20

OZ8194 PRELIMINARY; PRF; 142 AA.

ID C28194

AC C28194; PRELIMINARY; PRF; 142 AA.

DT 01-JAN-1998 (TEMBLrel. 05, Created)

DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)

DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)

DE Oxaloacetate decarboxylase, biotin carboxyl carrier subunit, putative.

GN AF2085.

OS Archaeoglobus fulgidus.

OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;

OCC Archaeoglobaceae; Archaeoglobus.

OX NCBI\_TaxID=2234;

RN [1]

RP SEQUENCE FROM N.A.

RR STRAIN=VC-16 / DSM 4304 / ATCC 49558;

RX MEDLINE=98049343; PubMed=9389475;

RA Klek H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

RA Ketchum K.A., Dodson R.J., Winn M., Hickey E.K., Peterson J.D.,

RA Reichmann D.L., Kerlavage A.R., Graham D.E., Kyripides N.C.,

RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

RA Peterson S., Raich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uterback T.,

RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

RA Sadov P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,



RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,  
RA Venter J.C.;  
RT "The complete genome sequence of the hyperthermophilic, sulphate-  
RL reducing archaeon *Archaeoglobus fulgidus*.";  
RL Nature 390:364-370(1997).  
DR EMBL; AE000960; AAB89171.1; -.  
DR PIR; D69510; D69510.  
DR HSSP; P10802; 11YU.  
DR TIGR; AF2085; -.  
DR InterPro; IPR000089; Biotin lipoyl.  
DR Pfam; PF00364; Biotin\_lipoyl; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 142 AA; 15573 MW; 73439FBD49E469A1 CRC64;

Query Match 47.1%; Score 161; DB 17; Length 142;  
Best Local Similarity 50.8%; Pred. No. 4.5e-09;  
Matches 32; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

Qy 1 EGEIPAPLAGTGVSKILVKGDTVKAGQTVLVLEAMKMETEINAPTQDGKVKVLERDAV 60  
Db 70 ENAVTSMPLPGVVLKPKGKVRAGEPVVIVSMKXENEIVSTEGVVAELVKEGRI 129  
Qy 61 QGG 63  
Db 130 EAG 132

RESULT 21  
Q87U07 PRELIMINARY; PRT; 602 AA.

AC Q87U07;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Oxaloacetate decarboxylase, alpha subunit.  
GN OADA OR PSPT05510.  
OS Pseudomonas syringae (pv. tomato).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=323;  
[1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=DC3000;  
RA Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,  
RA Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,  
RA Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,  
RA Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidson T.,  
RA White O., Fraser C., Collier A.;  
RT "Complete sequence of *Pseudomonas syringae*.";  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE016876; AA058929.1; -.  
DR TIGR; PSPT05510; -.  
DR GO; GO:0003824; F:catalytic activity; IEA.  
DR GO; GO:0006520; P:amino acid metabolism; IEA.  
DR InterPro; IPR000891; Biotin\_lipoyl.  
DR InterPro; IPR000891; HMGL-like.  
DR InterPro; IPR003379; Pyc OADA.  
DR InterPro; IPR000634; S/T dehydratase\_BS.  
DR Pfam; PF00364; biotin\_lipoyl; 1.  
DR Pfam; PF00682; HMGL-like; 1.  
DR Pfam; PF02436; Pyc OADA; 1.  
DR PROSITE; PS00165; DEHYDRATASE\_SER\_THR; 1.  
KW Complete proteome.  
SQ SEQUENCE 602 AA; 65598 MW; B0644376294712E3 CRC64;

Query Match 46.8%; Score 160; DB 16; Length 602;  
Best Local Similarity 48.5%; Pred. No. 3e-08;  
Matches 33; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

Qy 2 GEIPAPLAGTGVSKILVKGDTVKAGQTVLVLEAMKMETEINAPTQDGKVKVLERDAVQ 61  
Db 533 GHVSTTPGNIVDLVLEKGVVKGQAVLITEAMKMETEQVASTAGKVAIHVAKGRDVRN 592

Qy 62 GGOGLIKI 69  
Db 593 PGEILVEI 600  
PRELIMINARY; PRT; 576 AA.  
Q8U917  
AC Q8U917;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Biotin carboxylase.  
GN AU3913 OR AGR L 1864.  
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.  
OX NCBI\_TaxID=176299;  
[1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=21608550; PubMed=11743193;  
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,  
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,  
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,  
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,  
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,  
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,  
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,  
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,  
RA Nester E.W.;  
RT "The genome of the natural genetic engineer *Agrobacterium tumefaciens*  
C58.";  
RL Science 294:2317-2323(2001).  
[2]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=21608551; PubMed=11743194;  
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,  
RA Qurollo B., Goldman B.S., Cao Y., Akenazi M., Halling C., Mullin L.,  
RA Houmel K., Gordon J., Vaudin M., Tarchouk O., Epp A., Liu F.,  
RA Wollam C., Allinger M., Boughton D., Scott C., Lappas C., Markelz B.,  
RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,  
RA Cielo C., Slater S.;  
RT "Genome sequence of the plant pathogen and biotechnology agent  
Agrobacterium tumefaciens C58.";  
RL Science 294:2323-2328(2001).  
DR EMBL; AE009322; AAL44721.1; -.  
DR EMBL; AE008292; AAK89506.1; -.  
DR PIR; AC3038; AC3038.  
DR PIR; H98247; H98247.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:000374; F:biotin binding; IEA.  
DR GO; GO:0016874; F:ligase activity; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR InterPro; IPR001882; Biotin BS.  
DR InterPro; IPR005482; Biotin carb C.  
DR InterPro; IPR000089; Biotin\_lipoyl.  
DR InterPro; IPR005479; CPase\_L\_D2.  
DR InterPro; IPR005481; CPase\_L\_N.  
DR Pfam; PF02785; Biotin\_carb\_C; 1.  
DR Pfam; PF00364; biotin\_lipoyl; 1.  
DR Pfam; PF00289; CPase\_L chain; 1.  
DR Pfam; PF02786; CPase\_L\_D2; 1.  
DR PROSITE; PS00188; BIOTIN; 1.  
DR PROSITE; PS00867; CPSASE\_2; 1.  
KW Complete proteome.  
SQ SEQUENCE 576 AA; 61722 MW; E0299479A952581F CRC64;

Query Match 46.6%; Score 159.5; DB 16; Length 576;  
Best Local Similarity 50.7%; Pred. No. 3.2e-08;  
Matches 35; Conservative 13; Mismatches 20; Indels 1; Gaps 1;  
Qy 1 EGEIPAPLAGTGVSKILVKGDTVKAGQTVLVLEAMKMETEINAPTQDGKVKVLERDAV 60

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Db 507 EGEATPVSQTQSFVKDGETVSGDGLLAWMEAMKMETQIVATRAGKV-RLIVKEGDYL 565
QY 61 QGGGLIKI 69
Db 566 QAGATLIDI 574

RESULT 23
Q8A737 PRELIMINARY; PRT; 144 AA.
AC Q8A737;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Biotin carboxyl carrier protein (BCCP).
GN Btl688.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RT Chiang H.C., Hooper L.V., Gordon J.I.;
RL "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
DR Science 299:2074-2076(2003).
DR EMBL: AE016932; AA076795.1; -.
DR GO: GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
DR GO: GO:0003959; F:acetyl-CoA carboxylase activity; IEA.
DR GO: GO:0009374; F:biotin binding; IEA.
DR GO: GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro: IPR001249; AcCoA_biotinCC.
DR InterPro: IPR001882; Biotin_BS.
DR InterPro: IPR000089; Biotin_lipoyl.
DR Pfam: PF00364; biotin_lipoyl; 1.
DR PRINTS: PR01071; ACOABTINCC.
DR PROSITE: PS00188; BIOTIN; 1.
KW Complete proteome.
SQ SEQUENCE 144 AA; 15487 MW; 462383E2FB85601E CRC64;

Query Match 46.5%; Score 159; DB 16; Length 144;
Best Local Similarity 50.0%; Pred. No. 7.3e-09;
Matches 33; Conservative 10; Mismatches 23; Indels 0; Gaps 0;

QY 4 IPAPLAGTQSKLVKGGDTVKAGTQVLVLEAMKMETEINAPTDGKVEKVLKRDVQGG 63
Db 78 VKSLPGVILDIKVVNGDVKRGQTIIILEAMKMNINADKDKVTAINVNGDSVLEG 137
QY 64 QGLIKI 69
Db 138 NDLVII 143

RESULT 24
Q88C37 PRELIMINARY; PRT; 602 AA.
AC Q88C37;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Oxaloacetate decarboxylase, alpha subunit.
GN OADA OR PP5346.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
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RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Meazzaz A.,
RA Uterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
RA Lauber J., Stjepandic D., Hobeisel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J., Timmis K.N., Duesternoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL: AE016794; AA070911.1; -.
DR TIGR: PF5346; -.
DR GO: GO:0003824; F:catalytic activity; IEA.
DR GO: GO:0006520; P:amino acid metabolism; IEA.
DR InterPro: IPR000089; Biotin_lipoyl.
DR InterPro: IPR000891; HMGL-like.
DR InterPro: IPR001379; PYC OADA.
DR InterPro: IPR000634; S/T_dehydrtse_BS.
DR Pfam: PF00364; biotin_lipoyl; 1.
DR Pfam: PF00682; HMGL-like; 1.
DR Pfam: PF02436; PYC OADA; 1.
DR PROSITE: PS00165; DEHYDRATASE_SER_THR; 1.
KW Complete proteome.
SQ SEQUENCE 602 AA; 65626 MW; 98552963F0B691A7 CRC64;

Query Match 46.5%; Score 159; DB 16; Length 602;
Best Local Similarity 50.0%; Pred. No. 3.8e-08;
Matches 34; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

QY 2 GEIPAPLAGTQSKLVKGGDTVKAGTQVLVLEAMKMETEINAPTDGKVEKVLKRDVQ 61
Db 533 GHVSTMPGNIVDLVLEKGMVKAGQAVLITEAMKMETEVQAAIAGKVVAHVAKGRVT 592
QY 62 QGGGLIKI 69
Db 593 PGEILIEI 600

RESULT 25
Q92H13 PRELIMINARY; PRT; 665 AA.
AC Q92H13;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Propionyl-CoA carboxylase alpha chain.
GN PCCA OR RC0959.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
DR EMBL: AE008649; AA03497.1; -.
DR PIR: G97819; G97819.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0009374; F:biotin binding; IEA.
DR GO: GO:0016874; F:ligase activity; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR001882; Biotin_BS.
DR InterPro: IPR005482; Biotin_carb_C.
DR InterPro: IPR000089; Biotin_lipoyl.
DR InterPro: IPR005479; Cphase_L_D2.
DR InterPro: IPR005481; Cphase_L_N.
DR Pfam: PF02785; Biotin_carb_C; 1.
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DR Pfam; PF00364; biotin lipoyl; 1.
DR Pfam; PF00289; CPSase_L chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00866; CPSASE_1; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
DR Complete proteome.
KW SEQUENCE 665 AA; 73320 MW; 3054C1E18E0C14A3 CRC64;

Query Match
Best Local Similarity 46.5%; Score 159; DB 16; Length 665;
Matches 33; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 3 EIPAPLAGTVSKILVKEGTVKAGQTVLVLEAMKMETEINAPTDGKVKVVKERDAVG 62
DB 598 ELCAPLSGQIAIKVKEGQEVTAAGGEIMLTAMKNLILARDQIAKIFWKNVIR 657
QY 63 GGGLIK 68
DB 658 GQVILE 663

RESULT 26
QY74R8 PRELIMINARY; PRT; 169 AA.
AC QY74R8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative biotin carboxyl carrier protein.
GN ST0592.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus
OX NCBI_TaxID=111955;
RN SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Anka A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain 7.";
RL DNA Res. 8:123-140(2001).
DR EMBL; AP000983; BAB65589.1;
DR InterPro; IPR000089; Biotin lipoyl.
DR Pfam; PF00364; biotin lipoyl; 1.
DR Hypothetical protein; Complete proteome.
KW SEQUENCE 169 AA; 18839 MW; 4FID96761F5BE3DD CRC64;

Query Match
Best Local Similarity 46.2%; Score 158; DB 17; Length 169;
Matches 34; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

QY 1 EGEIPAPLAGTVSKILVKEGTVKAGQTVLVLEAMKMETEINAPTDGKVKVVKERDAV 60
DB 100 EGEILSPQGRIVQIRVKEGDAVKNKGQPLLSIEMKSETVISAPVGGVQKIMVKGQGV 159
QY 61 QGGQGLIKI 69
DB 160 KGGLLILLI 168

RESULT 27
QYHTD1 PRELIMINARY; PRT; 607 AA.
AC QYHTD1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Probable transcarboxylase subunit.
GN PA5435.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
EL Nature 405:959-964(2000).
DR EMBL; AB004956; AAG08820.1; -.
DR PIR; F82966; F82966.
DR HSSP; P02905; 3BDO.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008948; F:oxaloacetate decarboxylase activity; IEA.
DR GO; GO:0006520; P:amino acid metabolism; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR000089; Biotin lipoyl.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR005776; Oada.
DR InterPro; IPR003379; PYC OADA.
DR InterPro; IPR000634; S/T dehydratase_BS.
DR Pfam; PF00364; biotin lipoyl; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC OADA; 1.
DR TIGRfams; TIGR01108; oada; 1.
DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
DR Complete proteome.
KW SEQUENCE 607 AA; 66095 MW; 232AB0E9B935E010 CRC64;

Query Match
Best Local Similarity 46.2%; Score 158; DB 16; Length 607;
Matches 33; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

QY 2 GEIPAPLAGTVSKILVKEGTVKAGQTVLVLEAMKMETEINAPTDGKVKVVKERDAVQ 61
DB 538 GHVSTMPGNIVDLVLEKGSVKAGQAVLITEAMKMETEVQAGIAGTVKAIHVAKGRVN 597
QY 62 GGQGLIKI 69
DB 598 PGEILLIEI 605

RESULT 28
QY2CW1 PRELIMINARY; PRT; 1146 AA.
AC QY2CW1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PyCA protein.
GN PYCA OR LIN1060.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537229; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloecher H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

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[illegible]

DR GO: 0005524; F:ATP binding; IEA.  
 DR GO: 0016874; F:ligase activity; IEA.  
 DR GO: 0004736; F:pyruvate carboxylase activity; IEA.  
 DR GO: 0006094; P:gluconeogenesis; IEA.  
 DR GO: 0008152; P:metabolism; IEA.  
 DR InterPro: IPR005482; Biotin carb C.  
 DR InterPro: IPR000089; Biotin lipoyl.  
 DR InterPro: IPR005479; Case\_L\_D2.  
 DR InterPro: IPR005481; Case\_L\_N.  
 DR InterPro: IPR000891; HMGL-like.  
 DR InterPro: IPR003379; PYC OADA.  
 DR InterPro: IPR005930; Pyruv carbox.  
 DR Pfam: PF02785; Biotin carb C; 1.  
 DR Pfam: PF00364; biotin\_lipoyl; 1.  
 DR Pfam: PF00289; CPsase\_L\_chain; 1.  
 DR Pfam: PF02786; CPsase\_L\_D2; 1.  
 DR Pfam: PF00682; HMGL-like; 1.  
 DR Pfam: PF02436; HMGL-like; 1.  
 DR TIGRFAMs: TIGR01235; pyruv carbox; 1.  
 DR PROSITE: PS00867; CPsase\_2; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 1150 AA; ED67898E8A9F3BD4 CRC64;  
 Query Match 45.9%; Score 157; DB 16; Length 1150;  
 Best Local Similarity 50.0%; Pred. No. 1.3e-07;  
 Matches 33; Conservative 13; Mismatches 20; Indels 0; Gaps 0;  
 QY 4 IPAPLAGTQSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVLEKRDVQGG 63  
 Db 1082 IGASMPGTQVKALVEKGVKQGDHLMITEAMKMETTVQAPFDGEVVALVHKGDGAIQTG 1141  
 QY 64 QGLIKI 69  
 Db 1142 DLLIEV 1147  
 RESULT 31  
 Q8L2G4 PRELIMINARY; PRT; 1140 AA.  
 AC Q8L2G4  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Pyruvate carboxylase.  
 GN PYC.  
 OS Corynebacterium crenatum.  
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;  
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
 CX NCBI\_TaxID=168810;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CD945;  
 RA Wang J., Ding J., Liu Y.;  
 RT "Cloning and Expression of Pyruvate Carboxylase Gene in  
 Corynebacterium crenatum CD945";  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF503915; AA27458.1; -  
 DR GO: 0005737; C:cytoplasm; IEA.  
 DR GO: 0005524; F:ATP binding; IEA.  
 DR GO: 0009374; F:biotin binding; IEA.  
 DR GO: 0016874; F:ligase activity; IEA.  
 DR GO: 0004736; F:pyruvate carboxylase activity; IEA.  
 DR GO: 0006094; P:gluconeogenesis; IEA.  
 DR GO: 0008152; P:metabolism; IEA.  
 DR InterPro: IPR001882; Biotin BS.  
 DR InterPro: IPR005482; Biotin carb C.  
 DR InterPro: IPR000089; Biotin lipoyl.  
 DR InterPro: IPR005479; Case\_L\_D2.  
 DR InterPro: IPR005481; Case\_L\_N.  
 DR InterPro: IPR000891; HMGL-like.  
 DR InterPro: IPR003379; PYC OADA.  
 DR InterPro: IPR005930; Pyruv carbox.  
 DR Pfam: PF02785; Biotin carb C; 1.

DR Pfam: PF00364; biotin\_lipoyl; 1.  
 DR Pfam: PF00289; CPsase\_L\_chain; 1.  
 DR Pfam: PF02786; CPsase\_L\_D2; 1.  
 DR Pfam: PF00682; HMGL-like; 1.  
 DR Pfam: PF02436; PYC OADA; 1.  
 DR TIGRFAMs: TIGR01235; pyruv carbox; 1.  
 DR PROSITE: PS00188; Biotin; 1.  
 DR PROSITE: PS00867; CPsase\_2; 1.  
 SQ SEQUENCE 1140 AA; 123126 MW; FFA90BB7644C910E CRC64;  
 Query Match 45.8%; Score 156.5; DB 2; Length 1140;  
 Best Local Similarity 46.4%; Pred. No. 1.4e-07;  
 Matches 32; Conservative 13; Mismatches 23; Indels 1; Gaps 1;  
 QY 1 EGEIPAPLAGTQSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVLEKRDV 60  
 Db 1072 KGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIEMKMEATITASVDGKIDRVVVPATKV 1130  
 QY 61 QGGGLIKI 69  
 Db 1131 EGGDLIVV 1139  
 RESULT 32  
 Q99ZL6 PRELIMINARY; PRT; 116 AA.  
 AC Q99ZL6  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Putative methylmalonyl-CoA decarboxylase, gamma-subunit  
 DE EC 4.1.1.41.  
 GN SPY1176.  
 OS Streptococcus pyogenes.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 CX NCBI\_TaxID=1314;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SF370 / ATCC 700294 / Serotype M1;  
 MEDLINE=21192684; PubMed=11296296;  
 RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,  
 Primeaux C., Sezate S., Suvoarov A.N., Kenton S., Lai H.S., Lin S.P.,  
 Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,  
 Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;  
 RA "Complete genome sequence of an M1 strain of Streptococcus pyogenes";  
 RT Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).  
 CC -I- COFACTOR: BIOTIN (BY SIMILARITY).  
 DR EMBL; AE006558; AAK34043.1; -  
 DR HSP; P02905; 1BD0.  
 DR GO: 0009374; F:biotin binding; IEA.  
 DR GO: 0016829; F:lyase activity; IEA.  
 DR GO: 0004492; F:methylmalonyl-CoA decarboxylase activity; IEA.  
 DR InterPro: IPR001882; Biotin BS.  
 DR InterPro: IPR000089; Biotin lipoyl.  
 DR Pfam: PF00364; biotin\_lipoyl; 1.  
 DR PROSITE: PS00188; Biotin; 1.  
 KW Biotin; lyase; Complete proteome.  
 SQ SEQUENCE 116 AA; 12288 MW; A245219AC595BFECC CRC64;  
 Query Match 45.6%; Score 156; DB 16; Length 116;  
 Best Local Similarity 52.3%; Pred. No. 1.2e-08;  
 Matches 34; Conservative 7; Mismatches 24; Indels 0; Gaps 0;  
 QY 3 EIPAPLAGTQSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVLEKRDVQGG 62  
 Db 50 QVKAPMSGTVLISIFATGKAVKKGAEVLVLEAMKMEINILAPADGLVSKIHVVANQTVES 109  
 QY 63 GQGLI 67  
 Db 110 EQVLI 114

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RESULT 33
Q8K7G1
ID Q8K7G1 PRELIMINARY; PRT; 116 AA.
AC Q8K7G1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative methylmalonyl-CoA decarboxylase gamma-subunit.
GN SPYJ_0824 OR SPS1025.
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence."
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=SSI-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.;
RT "The genome of invasive Streptococcus pyogenes; a comparative analysis
RT of S. pyogenes SSI-1, SF370 and MGAS8232."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE014153; AAM79431.1; -.
DR EMBL; AP005144; BAC64120.1; -.
DR GO; GO:0009374; F:biotin binding; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR000089; Biotin_lipoyl.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR PROSITE; PS00188; BIOTIN; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 116 AA; 12260 MW; FC4BC174CB6BAFFA CRC64;

Query Match 45.6%; Score 156; DB 16; Length 116;
Best Local Similarity 52.3%; Pred. No. 1.2e-08;
Matches 34; Conservative 7; Mismatches 28; Indels 0; Gaps 0;

QY 3 EIPAPLAGTSKIIIVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVLERDAVQ 62
Db 50 QVXAPSGTVLSIFATGKAVKGEVILVLEAMKMETEINAPADGLVSKIHVVANQTVES 109
QY 63 GQGLI 67
Db 110 EQVLI 114

RESULT 34
Q8RQL2
ID Q8RQL2 PRELIMINARY; PRT; 1139 AA.
AC Q8RQL2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pyruvate carboxylase.
GN PYC.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
SEQUENCE FROM N.A.
RA Akiyoshi N., Nonaka G., Kimura E., Kawahara Y., Sugimoto S.;

RT "Corynebacterium efficiens pyruvate carboxylase (pyc) gene, complete
RT CDS."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- COFACTOR: BIOTIN (BY SIMILARITY).
DR EMBL; AB083299; BAB8903.1; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0004736; F:pyruvate carboxylase activity; IEA.
DR GO; GO:0006094; P:gluconeogenesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001882; Biotin_BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR000089; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC_OADA.
DR InterPro; IPR005930; PYruv carbox.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPase_L_chain; 1.
DR Pfam; PF02786; CPase_L_D2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRFAMs; TIGR01235; PYruv carbox; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00867; CPASE_2; 1.
KW Biotin.
SQ SEQUENCE 1139 AA; 123068 MW; BA7023134519FAAA CRC64;

Query Match 45.5%; Score 155.5; DB 2; Length 1139;
Best Local Similarity 43.5%; Pred. No. 1.8e-07;
Matches 30; Conservative 15; Mismatches 23; Indels 1; Gaps 1;

QY 1 EGEIPAPLAGTSKIIIVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVKVLERDAV 60
Db 1071 KGHVAAPFAGVVT-VTVASGDEIKAGDAVAIIAMKMETITAPVDGVIDRVVPAATKV 1129
QY 61 GQGQGLIKI 69
Db 1130 EGGDLIVV 1138

RESULT 35
OS4587
ID OS4587 PRELIMINARY; PRT; 1140 AA.
AC OS4587;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pyruvate carboxylase (EC 6.4.1.1).
GN PYC OR CGL0689.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=21253;
RA Koffas M.A.G., Ramamoorthi R., Pine W.A., Sinskey A.J.,
RA Stephanopoulos G.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032;
RA Peters-Wendisch P.G., Kreutzer C., Kalinowski J., Fatek M., Sahm H.,
RA Bickmanns B.J.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;

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RA Nakagawa S.;  
 RT "Complete genomic sequence of *Corynebacterium glutamicum* ATCC 13032.";  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 CC -|- COFACTOR: BIOTIN (BY SIMILARITY).  
 DR EMBL; AF038548; AAB92588.1; -;  
 DR EMBL; Y09548; CAA70739.1; -;  
 DR EMBL; AP005276; BAB98082.1; -;  
 DR HSP; P24182; 1BNC.  
 DR GO; GO:0005737; C:cytoplasm; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:000374; F:biotin binding; IEA.  
 DR GO; GO:0016874; F:ligase activity; IEA.  
 DR GO; GO:0004736; F:pyruvate carboxylase activity; IEA.  
 DR GO; GO:0006094; P:gluconeogenesis; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR InterPro; IPR005479; CPase\_L\_D2.  
 DR InterPro; IPR005481; CPase\_L\_N.  
 DR InterPro; IPR000891; HMGL-like.  
 DR InterPro; IPR003379; PYC OADA.  
 DR Pfam; PF02785; Biotin\_carb\_C; 1.  
 DR Pfam; PF00364; biotin\_lipoyl; 1.  
 DR Pfam; PF00289; CPSase\_L\_chain; 1.  
 DR Pfam; PF02786; CPSase\_L\_D2; 1.  
 DR Pfam; PF00682; HMGL-like; 1.  
 DR Pfam; PF02436; PYC OADA; 1.  
 DR TIGRfams; TIGR01235; pyruv\_carbox; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 DR PROSITE; PS00867; CPSASE\_2; 1.  
 DR Biotin; Ligase; Pyruvate; Complete proteome.  
 KW Biotin; Ligase; Pyruvate; Complete proteome.  
 SQ SEQUENCE 1140 AA; 123102 MW; 2A6D4B4ED2FEB531 CRC64;  
 Query Match 45.5%; Score 155.5; DB 16; Length 1140;  
 Best Local Similarity 44.9%; Pred. No. 1.8e-07;  
 Matches 31; Conservative 14; Mismatches 23; Indels 1; Gaps 1;  
 Qy 1 EGEIPAPLAGTVSKILVKGEGTVKAGQTVLVEAKMTEINAPDTGKVKLVKRDV 60  
 Db 1072 KGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIEAKMTEITASVDGKIDRVVVPAAATKV 1130  
 Qy 61 QGGQGLIKI 69  
 Db 1131 EGGDLIVV 1139  
 RESULT 36  
 Q8FRQO PRELIMINARY; PRT; 1168 AA.  
 AC Q8FRQO;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Pyruvate carboxylase (EC 6.4.1.1).  
 GN PYC OR CE0709.  
 OS *Corynebacterium efficiens*.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
 OX NCBI\_TaxID=152794;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;  
 RA Kawabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,  
 RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,  
 RA Usuda Y., Sugimoto S.;  
 RT "The entire genomic sequence of *Corynebacterium efficiens* YS-314.";  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AP005215; BAC17519.1; -;  
 DR GO; GO:0005737; C:cytoplasm; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:000374; F:biotin binding; IEA.

DR GO; GO:0016874; F:ligase activity; IEA.  
 DR GO; GO:0004736; F:pyruvate carboxylase activity; IEA.  
 DR GO; GO:0006094; P:gluconeogenesis; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR InterPro; IPR000089; Biotin\_lipoyl.  
 DR InterPro; IPR005479; CPase\_L\_D2.  
 DR InterPro; IPR005481; CPase\_L\_N.  
 DR InterPro; IPR000891; HMGL-like.  
 DR InterPro; IPR003379; PYC OADA.  
 DR Pfam; PF02785; Biotin\_carb\_C; 1.  
 DR Pfam; PF00364; biotin\_lipoyl; 1.  
 DR Pfam; PF00289; CPSase\_L\_chain; 1.  
 DR Pfam; PF02786; CPSase\_L\_D2; 1.  
 DR Pfam; PF00682; HMGL-like; 1.  
 DR Pfam; PF02436; PYC OADA; 1.  
 DR TIGRfams; TIGR01235; pyruv\_carbox; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 DR PROSITE; PS00867; CPSASE\_2; 1.  
 DR Ligase; Complete proteome.  
 KW Ligase; Complete proteome.  
 SQ SEQUENCE 1168 AA; 126245 MW; A5D5A4DD4DF285F8 CRC64;  
 Query Match 45.5%; Score 155.5; DB 16; Length 1168;  
 Best Local Similarity 43.5%; Pred. No. 1.9e-07;  
 Matches 30; Conservative 15; Mismatches 23; Indels 1; Gaps 1;  
 Qy 1 EGEIPAPLAGTVSKILVKGEGTVKAGQTVLVEAKMTEINAPDTGKVKLVKRDV 60  
 Db 1100 KGHVAAPFAGVVT-VTVAEGDEIKAGDAVAIEAKMTEITAPVDGVIDRVVVPAAATKV 1158  
 Qy 61 QGGQGLIKI 69  
 Db 1159 EGGDLIVV 1167  
 RESULT 37  
 Q8P104 PRELIMINARY; PRT; 116 AA.  
 AC Q8P104;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Putative methylmalonyl-CoA decarboxylase, gamma-subunit.  
 GN SPYM18.1128.  
 OS *Streptococcus pyogenes* (serotype M18).  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=186103;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MGAS8232 / Serotype M18;  
 RX MEDLINE=21927593; PubMed=11917108;  
 RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,  
 RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,  
 RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,  
 RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;  
 RT "Genome sequence and comparative microarray analysis of serotype M18  
 RT group A *Streptococcus* strains associated with acute rheumatic fever  
 RT outbreaks.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).  
 DR EMBL; AE010038; AAL97749.1; -;  
 DR GO; GO:000374; F:biotin binding; IEA.  
 DR InterPro; IPR001882; Biotin\_BS.  
 DR Pfam; PF00364; biotin\_lipoyl; 1.  
 DR PROSITE; PS00188; BIOTIN; 1.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 116 AA; 12290 MW; FC4BDE49CB6BAFFA CRC64;  
 Query Match 45.3%; Score 155; DB 16; Length 116;  
 Best Local Similarity 52.3%; Pred. No. 1.5e-08;

Matches 34; Conservative 7; Mismatches 24; Indels 0; Gaps 0;

QY 3 EIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVKVLEKRDVAG 62  
:::|||||  
Db 50 QVKAPMSGTVLSIFATGKAVKKEGAIVLEAMKMETEILAPDGLVSKIHVVANQWVS 109  
QY 63 GQGLI 67  
Db 110 EQVLI 114

RESULT 38  
Q8RAJ2 PRELIMINARY; PRT; 135 AA.

AC Q8RAJ2;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Biotin carboxyl carrier protein.  
GN ACCB OR TTE122.  
OS Thermoanaerobacter tengcongensis.  
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;  
OC Thermoanaerobacteriaceae; Thermoanaerobacter.  
OX NCBI\_TaxID=119072;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MB4 / JCM 11007;  
RX MEDLINE=21992816; PubMed=1197336;  
RA Bao Q., Tian Y., Li W., Xu Z., Huang Z., Hu S., Dong W., Yang J.,  
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,  
RA Tan H., Chen R., Wang J., Yu J., Yang H.,  
RT "A complete sequence of T. tengcongensis genome."  
RL Genome Res. 12:689-700(2002).  
DR EMBL; AS013084; AAM24452.1;  
DR GO; GO:000374; F:biotin binding; IEA.  
DR InterPro; IPR001882; Biotin\_BS.  
DR InterPro; IPR000089; Biotin\_lipoyl.  
DR Pfam; PF00364; biotin\_lipoyl; 1.  
DR PROSITE; PS00188; biotin\_lipoyl; 1.  
DR PROSITE; PS00188; Biotin; 1.  
KW Complete proteome.  
SQ SEQUENCE 135 AA; 15195 MW; 9C2BF717C008800A CRC64;

Query Match 44.7%; Score 153; DB 16; Length 135;  
Best Local Similarity 47.8%; Pred. No. 2.9e-08;  
Matches 33; Conservative 11; Mismatches 23; Indels 2; Gaps 1;

QY 1 EGE--IPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVKVLEKRD 58  
|||||  
Db 64 EGEKTIAPMGITVDVRVKEGDKVKGDDVILEAMKMETEINAPENGTVSVNVAKGD 123  
QY 59 AVQGGQGLI 67  
Db 124 TVNRGDIIIV 132

RESULT 39  
O67544  
ID O67544 PRELIMINARY; PRT; 620 AA.  
AC O67544;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Oxaloacetate decarboxylase alpha chain.  
GN OADA OR AQ1614.  
OS Aquifex aeolicus.  
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.  
OX NCBI\_TaxID=63363;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VFS;  
RX MEDLINE=98196666; PubMed=9537320;  
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,  
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,

RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;  
RT "The complete genome of the hyperthermophilic bacterium Aquifex  
aeolicus";  
RL Nature 392:353-358(1998).  
DR EMBL; AE000747; AAC07497.1; -.  
DR PIR; F70439; F70439.  
DR HSP; P02905; 1BDO.  
DR GO; GO:0005874; C:microtubule; IEA.  
DR GO; GO:000374; F:biotin binding; IEA.  
DR GO; GO:0003824; F:catalytic activity; IEA.  
DR GO; GO:0005525; F:GTP binding; IEA.  
DR GO; GO:0008948; F:oxaloacetate decarboxylase activity; IEA.  
DR GO; GO:0007018; P:microtubule-based movement; IEA.  
DR GO; GO:0006814; P:sodium ion transport; IEA.  
DR InterPro; IPR002453; Beta\_tubulin.  
DR InterPro; IPR001882; Biotin\_BS.  
DR InterPro; IPR000089; Biotin\_lipoyl.  
DR InterPro; IPR000891; HMGL-like.  
DR InterPro; IPR005776; Oada.  
DR InterPro; IPR003379; PYC\_OADA.  
DR Pfam; PF00364; biotin\_lipoyl; 1.  
DR Pfam; PF00682; HMGL-like; 1.  
DR Pfam; PF02436; PYC\_OADA; 1.  
DR TIGRFAMs; TIGR01108; oada; 1.  
DR PROSITE; PS00188; BIOTIN; 1.  
DR PROSITE; PS00228; TUBULIN\_B\_AUTOREG; 1.  
KW Complete proteome.  
SQ SEQUENCE 620 AA; 70416 MW; 4F306D48794AE859 CRC64;

Query Match 44.7%; Score 153; DB 16; Length 620;  
Best Local Similarity 45.6%; Pred. No. 1.6e-07;  
Matches 31; Conservative 14; Mismatches 23; Indels 0; Gaps 0;

QY 2 GEIPAPLAGTVSKILVKEGDTVKGQTVLVLEAMKMETEINAPTDGKVKVLEKRDVAG 61  
:::|||||  
Db 545 GDVTSPTGKVVNIKNVGVGDEVKEGDLVLEAMKMETEINAPDGVGVVEIFVRVGETVN 604  
QY 62 GQGLI 69  
Db 605 PDEVLI 612

RESULT 40  
O52603 PRELIMINARY; PRT; 167 AA.  
ID O52603  
AC O52603 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Biotin carboxyl carrier protein.  
GN ACCB.  
OS Sulfolobus metallicus.  
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
OC Sulfolobus.  
OX NCBI\_TaxID=47303;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LM;  
RX MEDLINE=20059326; PubMed=10591844;  
RA Burton N.P., Williams T.D., Norris P.R.;  
RT "Carboxylase genes of Sulfolobus metallicus";  
RL Arch. Microbiol. 172:349-353(1999).  
DR EMBL; AF042099; AAB97085.1; -.  
DR PIR; T44291; T44291.  
DR HSP; P02905; 1BDO.  
DR InterPro; IPR000089; Biotin\_lipoyl.  
DR Pfam; PF00364; biotin\_lipoyl; 1.  
SQ SEQUENCE 167 AA; 18580 MW; F05A04F38BC55B09 CRC64;

Query Match 44.4%; Score 152; DB 1; Length 167;  
Best Local Similarity 50.7%; Pred. No. 4.7e-08;  
Matches 34; Conservative 9; Mismatches 24; Indels 0; Gaps 0;



